



SEQUENCE LISTING

#4
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<110> Rikihisa, Yasuko
Ohasi, Norio

<120> Outer Membrane Protein of Ehrlichia Canis and Ehrlichia
Chaffeensis

<130> 22727/04021

<140> 09/314,701

<141> 1999-05-19

<160> 66

<170> PatentIn Ver. 2.0

<210> 1

<211> 846

<212> DNA

<213> Ehrlichia chaffeensis

<220>

<221> CDS

<222> (1)..(846)

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tct tct cta cct gga gta tca ttt tcc gac cca gca ggt agt ggt att	96
Ser Ser Leu Pro Gly Val Ser Phe Ser Asp Pro Ala Gly Ser Gly Ile	
20 25 30	

aac ggt aat ttc tac atc agt gga aaa tac atg cca agt gct tcg cat	144
Asn Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro Ser Ala Ser His	
35 40 45	

ttt gga gta ttc tct gct aag gaa gaa aga aat aca aca gtt gga gtg	192
Phe Gly Val Phe Ser Ala Lys Glu Glu Arg Asn Thr Thr Val Gly Val	
50 55 60	

ttt gga ctg aag caa aat tgg gac gga agc gca ata tcc aac tcc tcc	240
Phe Gly Leu Lys Gln Asn Trp Asp Gly Ser Ala Ile Ser Asn Ser Ser	
65 70 75 80	

cca aac gat gta ttc act gtc tca aat tat tca ttt aaa tat gaa aac	288

Pro	Asn	Asp	Val	Phe	Thr	Val	Ser	Asn	Tyr	Ser	Phe	Lys	Tyr	Glu	Asn		
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Asn	Pro	Phe	Leu	Gly	Phe	Ala	Gly	Ala	Ile	Gly	Tyr	Ser	Met	Asp	Gly		
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Pro	Arg	Ile	Glu	Leu	Glu	Val	Ser	Tyr	Glu	Thr	Phe	Asp	Val	Lys	Asn		
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caa	ggg	aac	aat	tat	aag	aat	gaa	gca	cat	aga	tat	tgt	gct	cta	tcc	432	
Gln	Gly	Asn	Asn	Tyr	Lys	Asn	Glu	Ala	His	Arg	Tyr	Cys	Ala	Leu	Ser		
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cat	aac	tca	gca	gca	gac	atg	agt	agt	gca	agt	aat	aat	ttt	gtc	ttt	480	
His	Asn	Ser	Ala	Ala	Asp	Met	Ser	Ser	Ala	Ser	Asn	Asn	Phe	Val	Phe		
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Leu	Lys	Asn	Glu	Gly	Leu	Leu	Asp	Ile	Ser	Phe	Met	Leu	Asn	Ala	Cys		
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Tyr	Asp	Val	Val	Gly	Glu	Gly	Ile	Pro	Phe	Ser	Pro	Tyr	Ile	Cys	Ala		
				180				185						190			
ggg	atc	ggg	act	gat	tta	gta	tcc	atg	ttt	gaa	gct	aca	aat	cct	aaa	624	
Gly	Ile	Gly	Thr	Asp	Leu	Val	Ser	Met	Phe	Glu	Ala	Thr	Asn	Pro	Lys		
			195				200					205					
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Ile	Ser	Tyr	Gln	Gly	Lys	Leu	Gly	Leu	Ser	Tyr	Ser	Ile	Ser	Pro	Glu		
			210				215					220					
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Ala	Ser	Val	Phe	Ile	Gly	Gly	His	Phe	His	Lys	Val	Leu	Gly	Asn	Glu		
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ttt	aga	gat	att	cct	act	ata	ata	cct	act	gga	tca	aca	ctt	gca	gga	768	
Phe	Arg	Asp	Ile	Pro	Thr	Ile	Ile	Pro	Thr	Gly	Ser	Thr	Leu	Ala	Gly		
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aaa	gga	aac	tac	cct	gca	ata	gta	ata	ctg	gat	gta	tgc	cac	ttt	gga	816	
Lys	Gly	Asn	Tyr	Pro	Ala	Ile	Val	Ile	Leu	Asp	Val	Cys	His	Phe	Gly		
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<210> 2

<211> 281

<212> PRT

<213> Ehrlichia chaffeensis

<400> 2

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Ser Ser Leu Pro Gly Val Ser Phe Ser Asp Pro Ala Gly Ser Gly Ile
20 25 30

Asn Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro Ser Ala Ser His
35 40 45

Phe Gly Val Phe Ser Ala Lys Glu Glu Arg Asn Thr Thr Val Gly Val
50 55 60

Phe Gly Leu Lys Gln Asn Trp Asp Gly Ser Ala Ile Ser Asn Ser Ser
65 70 75 80

Pro Asn Asp Val Phe Thr Val Ser Asn Tyr Ser Phe Lys Tyr Glu Asn
85 90 95

Asn Pro Phe Leu Gly Phe Ala Gly Ala Ile Gly Tyr Ser Met Asp Gly
100 105 110

Pro Arg Ile Glu Leu Glu Val Ser Tyr Glu Thr Phe Asp Val Lys Asn
115 120 125

Gln Gly Asn Asn Tyr Lys Asn Glu Ala His Arg Tyr Cys Ala Leu Ser
130 135 140

His Asn Ser Ala Ala Asp Met Ser Ser Ala Ser Asn Asn Phe Val Phe
145 150 155 160

Leu Lys Asn Glu Gly Leu Leu Asp Ile Ser Phe Met Leu Asn Ala Cys
165 170 175

Tyr Asp Val Val Gly Glu Gly Ile Pro Phe Ser Pro Tyr Ile Cys Ala
180 185 190

Gly Ile Gly Thr Asp Leu Val Ser Met Phe Glu Ala Thr Asn Pro Lys
195 200 205

Ile Ser Tyr Gln Gly Lys Leu Gly Leu Ser Tyr Ser Ile Ser Pro Glu
 210 215 220

Ala Ser Val Phe Ile Gly Gly His Phe His Lys Val Leu Gly Asn Glu
 225 230 235 240

Phe Arg Asp Ile Pro Thr Ile Ile Pro Thr Gly Ser Thr Leu Ala Gly
 245 250 255

Lys Gly Asn Tyr Pro Ala Ile Val Ile Leu Asp Val Cys His Phe Gly
 260 265 270

Ile Glu Leu Gly Gly Arg Phe Ala Phe
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<210> 3

<211> 852

<212> DNA

<213> Ehrlichia chaffeensis

<220>

<221> CDS

<222> (1)..(852)

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 1 5 10 15

tca atc tta cct tac caa tct ttt gca gat cct gta act tca aat gat 96
 Ser Ile Leu Pro Tyr Gln Ser Phe Ala Asp Pro Val Thr Ser Asn Asp
 20 25 30

aca gga atc aac gac agc aga gaa ggc ttc tac att agt gta aag tat 144
 Thr Gly Ile Asn Asp Ser Arg Glu Gly Phe Tyr Ile Ser Val Lys Tyr
 35 40 45

aat cca agc ata tca cac ttc aga aaa ttc tca gct gaa gaa gct ccc 192
 Asn Pro Ser Ile Ser His Phe Arg Lys Phe Ser Ala Glu Glu Ala Pro
 50 55 60

atc aat gga aat act tct atc act aaa aag gtt ttc ggg ctg aaa aaa 240
 Ile Asn Gly Asn Thr Ser Ile Thr Lys Lys Val Phe Gly Leu Lys Lys
 65 70 75 80

gac gga gat ata gca caa tct gcg aat ttt aac agg aca gat cca gcc 288

Asp Gly Asp Ile Ala Gln Ser Ala Asn Phe Asn Arg Thr Asp Pro Ala
 85 90 95

ctc gag ttt cag aat aac cta ata tca gga ttc tca gga agt att ggt 336
 Leu Glu Phe Gln Asn Asn Leu Ile Ser Gly Phe Ser Gly Ser Ile Gly
 100 105 110

tat gct atg gat ggg cca aga ata gaa ctt gaa gct gca tac caa aaa 384
 Tyr Ala Met Asp Gly Pro Arg Ile Glu Leu Glu Ala Ala Tyr Gln Lys
 115 120 125

ttt gat gca aaa aat cct gac aac aat gac act aat agc ggt gac tac 432
 Phe Asp Ala Lys Asn Pro Asp Asn Asn Asp Thr Asn Ser Gly Asp Tyr
 130 135 140

tat aaa tac ttt gga cta tct cgt gaa gac gca ata gca gat aag aaa 480
 Tyr Lys Tyr Phe Gly Leu Ser Arg Glu Asp Ala Ile Ala Asp Lys Lys
 145 150 155 160

tat gtt gtc ctt aaa aat gaa ggc atc act ttt atg tca tta atg gtt 528
 Tyr Val Val Leu Lys Asn Glu Gly Ile Thr Phe Met Ser Leu Met Val
 165 170 175

aac act tgc tat gac att aca gct gaa gga gta cct ttc ata ccg tat 576
 Asn Thr Cys Tyr Asp Ile Thr Ala Glu Gly Val Pro Phe Ile Pro Tyr
 180 185 190

gca tgt gca ggt gta gga gca gac ctt ata aac gta ttt aag gat ttt 624
 Ala Cys Ala Gly Val Gly Ala Asp Leu Ile Asn Val Phe Lys Asp Phe
 195 200 205

aat tta aaa ttc tca tac caa ggg aaa ata ggt att agc tat cca atc 672
 Asn Leu Lys Phe Ser Tyr Gln Gly Lys Ile Gly Ile Ser Tyr Pro Ile
 210 215 220

aca cca gaa gtt tcc gct ttt att gga gga tac tac cac gga gtt ata 720
 Thr Pro Glu Val Ser Ala Phe Ile Gly Gly Tyr Tyr His Gly Val Ile
 225 230 235 240

gga aat aat ttt aac aaa ata cct gta ata aca cct gta gta tta gaa 768
 Gly Asn Asn Phe Asn Lys Ile Pro Val Ile Thr Pro Val Val Leu Glu
 245 250 255

gga gct cct caa aca aca tct gcg cta gta act att gac act gga tac 816
 Gly Ala Pro Gln Thr Thr Ser Ala Leu Val Thr Ile Asp Thr Gly Tyr
 260 265 270

ttt ggc gga gaa gtt gga gta agg ttc acc ttc tag 852

Phe Gly Gly Glu Val Gly Val Arg Phe Thr Phe
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<210> 4

<211> 283

<212> PRT

<213> Ehrlichia chaffeensis

<400> 4

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Thr Gly Ile Asn Asp Ser Arg Glu Gly Phe Tyr Ile Ser Val Lys Tyr
 35 40 45

Asn Pro Ser Ile Ser His Phe Arg Lys Phe Ser Ala Glu Glu Ala Pro
 50 55 60

Ile Asn Gly Asn Thr Ser Ile Thr Lys Lys Val Phe Gly Leu Lys Lys
 65 70 75 80

Asp Gly Asp Ile Ala Gln Ser Ala Asn Phe Asn Arg Thr Asp Pro Ala
 85 90 95

Leu Glu Phe Gln Asn Asn Leu Ile Ser Gly Phe Ser Gly Ser Ile Gly
 100 105 110

Tyr Ala Met Asp Gly Pro Arg Ile Glu Leu Glu Ala Ala Tyr Gln Lys
 115 120 125

Phe Asp Ala Lys Asn Pro Asp Asn Asn Asp Thr Asn Ser Gly Asp Tyr
 130 135 140

Tyr Lys Tyr Phe Gly Leu Ser Arg Glu Asp Ala Ile Ala Asp Lys Lys
 145 150 155 160

Tyr Val Val Leu Lys Asn Glu Gly Ile Thr Phe Met Ser Leu Met Val
 165 170 175

Asn Thr Cys Tyr Asp Ile Thr Ala Glu Gly Val Pro Phe Ile Pro Tyr
 180 185 190

Ala Cys Ala Gly Val Gly Ala Asp Leu Ile Asn Val Phe Lys Asp Phe
 195 200 205

Asn Leu Lys Phe Ser Tyr Gln Gly Lys Ile Gly Ile Ser Tyr Pro Ile
 210 215 220

Thr Pro Glu Val Ser Ala Phe Ile Gly Gly Tyr Tyr His Gly Val Ile
 225 230 235 240

Gly Asn Asn Phe Asn Lys Ile Pro Val Ile Thr Pro Val Val Leu Glu
 245 250 255

Gly Ala Pro Gln Thr Thr Ser Ala Leu Val Thr Ile Asp Thr Gly Tyr
 260 265 270

Phe Gly Gly Glu Val Gly Val Arg Phe Thr Phe
 275 280

<210> 5

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<212> DNA

<213> Ehrlichia chaffeensis

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<221> CDS

<222> (1)..(843)

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tct ttc tta cct gga ata tta ctt tct gaa cca gta caa gat gac agt 96
 Ser Phe Leu Pro Gly Ile Leu Leu Ser Glu Pro Val Gln Asp Asp Ser
 20 25 30

gtg agt ggc aat ttc tat att agt ggc aag tac atg cca agt gct tct 144
 Val Ser Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro Ser Ala Ser
 35 40 45

cat ttt gga gtt ttc tct gcc aaa gaa gaa aaa aat cct act gtc gcg 192
 His Phe Gly Val Phe Ser Ala Lys Glu Glu Lys Asn Pro Thr Val Ala
 50 55 60

ttg tat ggt ttg aaa caa gat tgg aac ggt gtt agt gct tca agt cat 240
 Leu Tyr Gly Leu Lys Gln Asp Trp Asn Gly Val Ser Ala Ser Ser His
 65 70 75 80

gct gat gcg gac ttt aat aac aaa ggt tat tct ttt aaa tac gaa aac 288

Ala Asp Ala Asp Phe Asn Asn Lys Gly Tyr Ser Phe Lys Tyr Glu Asn	
85 90 95	
aat cca ttt cta ggt ttt gca gga gct att ggt tat tca atg ggt ggt	336
Asn Pro Phe Leu Gly Phe Ala Gly Ala Ile Gly Tyr Ser Met Gly Gly	
100 105 110	
cca aga ata gag ttt gaa gtg tcc tat gaa aca ttt gac gtg aaa aat	384
Pro Arg Ile Glu Phe Glu Val Ser Tyr Glu Thr Phe Asp Val Lys Asn	
115 120 125	
caa ggt ggt aat tac aaa aat gat gct cac aga tac tgt gcc tta gat	432
Gln Gly Gly Asn Tyr Lys Asn Asp Ala His Arg Tyr Cys Ala Leu Asp	
130 135 140	
cgt aaa gca agc agc act aat gcc aca gct agt cac tac gtg cta cta	480
Arg Lys Ala Ser Ser Thr Asn Ala Thr Ala Ser His Tyr Val Leu Leu	
145 150 155 160	
aaa aat gaa gga cta ctt gat ata tca ctt atg ttg aat gca tgc tat	528
Lys Asn Glu Gly Leu Leu Asp Ile Ser Leu Met Leu Asn Ala Cys Tyr	
165 170 175	
gac gta gta agt gaa gga ata cct ttc tct cct tac ata tgt gca ggt	576
Asp Val Val Ser Glu Gly Ile Pro Phe Ser Pro Tyr Ile Cys Ala Gly	
180 185 190	
gtt ggt acc gat tta ata tcc atg ttt gaa gct ata aac cct aaa att	624
Val Gly Thr Asp Leu Ile Ser Met Phe Glu Ala Ile Asn Pro Lys Ile	
195 200 205	
tct tat caa gga aag tta ggt ttg agt tac tct ata aac cca gaa gct	672
Ser Tyr Gln Gly Lys Leu Gly Leu Ser Tyr Ser Ile Asn Pro Glu Ala	
210 215 220	
tct gtc ttt gtt ggt gga cat ttt cat aaa gtt gca ggt aat gaa ttc	720
Ser Val Phe Val Gly Gly His Phe His Lys Val Ala Gly Asn Glu Phe	
225 230 235 240	
agg gac att tct act ctt aaa gcg ttt gct aca cca tca tct gca gct	768
Arg Asp Ile Ser Thr Leu Lys Ala Phe Ala Thr Pro Ser Ser Ala Ala	
245 250 255	
act cca gac tta gca aca gta aca ctg agt gtg tgt cac ttt gga gta	816
Thr Pro Asp Leu Ala Thr Val Thr Leu Ser Val Cys His Phe Gly Val	
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gaa ctt gga gga aga ttt aac ttc taa	843

Glu Leu Gly Gly Arg Phe Asn Phe
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<210> 6

<211> 280

<212> PRT

<213> Ehrlichia chaffeensis

<400> 6

Met Asn Cys Lys Lys Phe Phe Ile Thr Thr Ala Leu Ala Leu Pro Met
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Ser Phe Leu Pro Gly Ile Leu Leu Ser Glu Pro Val Gln Asp Asp Ser
20 25 30

Val Ser Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro Ser Ala Ser
35 40 45

His Phe Gly Val Phe Ser Ala Lys Glu Glu Lys Asn Pro Thr Val Ala
50 55 60

Leu Tyr Gly Leu Lys Gln Asp Trp Asn Gly Val Ser Ala Ser Ser His
65 70 75 80

Ala Asp Ala Asp Phe Asn Asn Lys Gly Tyr Ser Phe Lys Tyr Glu Asn
85 90 95

Asn Pro Phe Leu Gly Phe Ala Gly Ala Ile Gly Tyr Ser Met Gly Gly
100 105 110

Pro Arg Ile Glu Phe Glu Val Ser Tyr Glu Thr Phe Asp Val Lys Asn
115 120 125

Gln Gly Gly Asn Tyr Lys Asn Asp Ala His Arg Tyr Cys Ala Leu Asp
130 135 140

Arg Lys Ala Ser Ser Thr Asn Ala Thr Ala Ser His Tyr Val Leu Leu
145 150 155 160

Lys Asn Glu Gly Leu Leu Asp Ile Ser Leu Met Leu Asn Ala Cys Tyr
165 170 175

Asp Val Val Ser Glu Gly Ile Pro Phe Ser Pro Tyr Ile Cys Ala Gly
180 185 190

Val Gly Thr Asp Leu Ile Ser Met Phe Glu Ala Ile Asn Pro Lys Ile
195 200 205

Ser Tyr Gln Gly Lys Leu Gly Leu Ser Tyr Ser Ile Asn Pro Glu Ala
 210 215 220

Ser Val Phe Val Gly Gly His Phe His Lys Val Ala Gly Asn Glu Phe
 225 230 235 240

Arg Asp Ile Ser Thr Leu Lys Ala Phe Ala Thr Pro Ser Ser Ala Ala
 245 250 255

Thr Pro Asp Leu Ala Thr Val Thr Leu Ser Val Cys His Phe Gly Val
 260 265 270

Glu Leu Gly Gly Arg Phe Asn Phe
 275 280

<210> 7

<211> 861

<212> DNA

<213> Ehrlichia chaffeensis

<220>

<221> CDS

<222> (1)..(861)

<400> 7

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tcc ttc tta cct gga ata tca ctt tct gat cca gta cag gat gac aac 96
 Ser Phe Leu Pro Gly Ile Ser Leu Ser Asp Pro Val Gln Asp Asp Asn
 20 25 30

att agt ggt aat ttc tac atc agt gga aag tat atg cca agc gct tcg 144
 Ile Ser Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro Ser Ala Ser
 35 40 45

cat ttt gga gtt ttt tct gcc aag gaa gaa aga aat aca aca gtt gga 192
 His Phe Gly Val Phe Ser Ala Lys Glu Glu Arg Asn Thr Thr Val Gly
 50 55 60

gta ttt gga ata gag caa gat tgg gat aga tgt gta ata tct aga acc 240
 Val Phe Gly Ile Glu Gln Asp Trp Asp Arg Cys Val Ile Ser Arg Thr
 65 70 75 80

act tta agc gat ata ttc acc gtt cca aat tat tca ttt aag tat gaa 288

Thr	Leu	Ser	Asp	Ile	Phe	Thr	Val	Pro	Asn	Tyr	Ser	Phe	Lys	Tyr	Glu	
				85					90						95	
aat	aat	cta	ttt	tca	gga	ttt	gca	gga	gct	att	ggc	tac	tca	atg	gat	336
Asn	Asn	Leu	Phe	Ser	Gly	Phe	Ala	Gly	Ala	Ile	Gly	Tyr	Ser	Met	Asp	
			100					105					110			
ggc	cca	aga	ata	gag	ctt	gaa	gta	tct	tat	gaa	gca	ttc	gat	gtt	aaa	384
Gly	Pro	Arg	Ile	Glu	Leu	Glu	Val	Ser	Tyr	Glu	Ala	Phe	Asp	Val	Lys	
			115				120					125				
aat	caa	ggt	aac	aat	tat	aag	aac	gaa	gca	cat	aga	tat	tat	gct	ctg	432
Asn	Gln	Gly	Asn	Asn	Tyr	Lys	Asn	Glu	Ala	His	Arg	Tyr	Tyr	Ala	Leu	
			130				135				140					
tcc	cat	ctt	ctc	ggc	aca	gag	aca	cag	ata	gat	ggg	gca	ggc	agt	gcg	480
Ser	His	Leu	Leu	Gly	Thr	Glu	Thr	Gln	Ile	Asp	Gly	Ala	Gly	Ser	Ala	
					150					155					160	
tct	gtc	ttt	cta	ata	aat	gaa	gga	cta	ctt	gat	aaa	tca	ttt	atg	ctg	528
Ser	Val	Phe	Leu	Ile	Asn	Glu	Gly	Leu	Leu	Asp	Lys	Ser	Phe	Met	Leu	
					165				170					175		
aac	gca	tgt	tat	gat	gta	ata	agt	gaa	ggc	ata	cct	ttt	tct	cct	tat	576
Asn	Ala	Cys	Tyr	Asp	Val	Ile	Ser	Glu	Gly	Ile	Pro	Phe	Ser	Pro	Tyr	
					180				185				190			
ata	tgt	gca	ggt	att	ggt	att	gat	tta	gta	tcc	atg	ttt	gaa	gct	ata	624
Ile	Cys	Ala	Gly	Ile	Gly	Ile	Asp	Leu	Val	Ser	Met	Phe	Glu	Ala	Ile	
			195				200					205				
aat	cct	aaa	att	tct	tat	caa	gga	aaa	tta	ggc	tta	agt	tac	cct	ata	672
Asn	Pro	Lys	Ile	Ser	Tyr	Gln	Gly	Lys	Leu	Gly	Leu	Ser	Tyr	Pro	Ile	
			210				215				220					
agc	cca	gaa	gct	tct	gtg	ttt	att	ggt	gga	cat	ttt	cat	aag	gtg	ata	720
Ser	Pro	Glu	Ala	Ser	Val	Phe	Ile	Gly	Gly	His	Phe	His	Lys	Val	Ile	
			225			230				235				240		
gga	aac	gaa	ttt	aga	gat	att	cct	act	atg	ata	cct	agt	gaa	tca	gcg	768
Gly	Asn	Glu	Phe	Arg	Asp	Ile	Pro	Thr	Met	Ile	Pro	Ser	Glu	Ser	Ala	
					245				250					255		
ctt	gca	gga	aaa	gga	aac	tac	cct	gca	ata	gta	aca	ctg	gac	gtg	ttc	816
Leu	Ala	Gly	Lys	Gly	Asn	Tyr	Pro	Ala	Ile	Val	Thr	Leu	Asp	Val	Phe	
			260					265					270			
tac	ttt	ggc	ata	gaa	ctt	gga	gga	agg	ttt	aac	ttc	caa	ctt	tga		861

Tyr Phe Gly Ile Glu Leu Gly Gly Arg Phe Asn Phe Gln Leu
 275 280 285

<210> 8

<211> 286

<212> PRT

<213> Ehrlichia chaffeensis

<400> 8

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Ser Phe Leu Pro Gly Ile Ser Leu Ser Asp Pro Val Gln Asp Asp Asn
 20 25 30

Ile Ser Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro Ser Ala Ser
 35 40 45

His Phe Gly Val Phe Ser Ala Lys Glu Glu Arg Asn Thr Thr Val Gly
 50 55 60

Val Phe Gly Ile Glu Gln Asp Trp Asp Arg Cys Val Ile Ser Arg Thr
 65 70 75 80

Thr Leu Ser Asp Ile Phe Thr Val Pro Asn Tyr Ser Phe Lys Tyr Glu
 85 90 95

Asn Asn Leu Phe Ser Gly Phe Ala Gly Ala Ile Gly Tyr Ser Met Asp
 100 105 110

Gly Pro Arg Ile Glu Leu Glu Val Ser Tyr Glu Ala Phe Asp Val Lys
 115 120 125

Asn Gln Gly Asn Asn Tyr Lys Asn Glu Ala His Arg Tyr Tyr Ala Leu
 130 135 140

Ser His Leu Leu Gly Thr Glu Thr Gln Ile Asp Gly Ala Gly Ser Ala
 145 150 155 160

Ser Val Phe Leu Ile Asn Glu Gly Leu Leu Asp Lys Ser Phe Met Leu
 165 170 175

Asn Ala Cys Tyr Asp Val Ile Ser Glu Gly Ile Pro Phe Ser Pro Tyr
 180 185 190

Ile Cys Ala Gly Ile Gly Ile Asp Leu Val Ser Met Phe Glu Ala Ile
 195 200 205

Asn Pro Lys Ile Ser Tyr Gln Gly Lys Leu Gly Leu Ser Tyr Pro Ile
210 215 220

Ser Pro Glu Ala Ser Val Phe Ile Gly Gly His Phe His Lys Val Ile
225 230 235 240

Gly Asn Glu Phe Arg Asp Ile Pro Thr Met Ile Pro Ser Glu Ser Ala
245 250 255

Leu Ala Gly Lys Gly Asn Tyr Pro Ala Ile Val Thr Leu Asp Val Phe
260 265 270

Tyr Phe Gly Ile Glu Leu Gly Gly Arg Phe Asn Phe Gln Leu
275 280 285

<210> 9

<211> 837

<212> DNA

<213> *Ehrlichia chaffeensis*

<220>

<221> CDS

<222> (1)..(837)

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1 5 10 15

tcc ttt cta cct gga ata tca ttt tct gat cca gtg caa ggt gac aat 96
Ser Phe Leu Pro Gly Ile Ser Phe Ser Asp Pro Val Gln Gly Asp Asn
20 25 30

att agt ggt aat ttc tat gtt agt ggc aag tat atg cca agt gct tcg 144
Ile Ser Gly Asn Phe Tyr Val Ser Gly Lys Tyr Met Pro Ser Ala Ser
35 40 45

cat ttt ggc atg ttt tct gcc aaa gaa gaa aaa aat cct act gtt gca 192
His Phe Gly Met Phe Ser Ala Lys Glu Glu Lys Asn Pro Thr Val Ala
50 55 60

ttg tat ggc tta aaa caa gat tgg gaa ggg att agc tca tca agt cac 240
Leu Tyr Gly Leu Lys Gln Asp Trp Glu Gly Ile Ser Ser Ser Ser His
65 70 75 80

aat gat aat cat ttc aat aac aag ggt tat tca ttt aaa tat gaa aat 288

Asn Asp Asn His Phe Asn Asn Lys Gly Tyr Ser Phe Lys Tyr Glu Asn	
85 90 95	
aac cca ttt tta ggg ttt gca gga gct att ggt tat tca atg ggt ggt	336
Asn Pro Phe Leu Gly Phe Ala Gly Ala Ile Gly Tyr Ser Met Gly Gly	
100 105 110	
cca aga gta gag ttt gaa gtg tcc tat gaa aca ttt gac gtt aaa aat	384
Pro Arg Val Glu Phe Glu Val Ser Tyr Glu Thr Phe Asp Val Lys Asn	
115 120 125	
cag ggt aat aac tat aaa aat gat gct cac aga tac tgt gct tta ggt	432
Gln Gly Asn Asn Tyr Lys Asn Asp Ala His Arg Tyr Cys Ala Leu Gly	
130 135 140	
caa caa gac aac agc gga ata cct aaa act agt aaa tac gta ctg tta	480
Gln Gln Asp Asn Ser Gly Ile Pro Lys Thr Ser Lys Tyr Val Leu Leu	
145 150 155 160	
aaa agc gaa gga ttg ctt gac ata tca ttt atg cta aat gca tgc tat	528
Lys Ser Glu Gly Leu Leu Asp Ile Ser Phe Met Leu Asn Ala Cys Tyr	
165 170 175	
gat ata ata aac gag agc ata cct ttg tct cct tac ata tgt gca ggt	576
Asp Ile Ile Asn Glu Ser Ile Pro Leu Ser Pro Tyr Ile Cys Ala Gly	
180 185 190	
gtt ggt act gat tta ata tcc atg ttt gaa gct aca aat cct aaa att	624
Val Gly Thr Asp Leu Ile Ser Met Phe Glu Ala Thr Asn Pro Lys Ile	
195 200 205	
tct tac caa ggg aag tta ggt cta agt tac tct ata aac cca gaa gct	672
Ser Tyr Gln Gly Lys Leu Gly Leu Ser Tyr Ser Ile Asn Pro Glu Ala	
210 215 220	
tct gta ttt att ggt gga cat ttt cat aag gtg ata gga aac gaa ttt	720
Ser Val Phe Ile Gly Gly His Phe His Lys Val Ile Gly Asn Glu Phe	
225 230 235 240	
agg gac att cct act ctg aaa gca ttt gtt acg tca tca gct act cca	768
Arg Asp Ile Pro Thr Leu Lys Ala Phe Val Thr Ser Ser Ala Thr Pro	
245 250 255	
gat cta gca ata gta aca cta agt gta tgt cat ttt gga ata gaa ctt	816
Asp Leu Ala Ile Val Thr Leu Ser Val Cys His Phe Gly Ile Glu Leu	
260 265 270	
gga gga agg ttt aac ttc taa	837

Gly Gly Arg Phe Asn Phe
275

<210> 10

<211> 278

<212> PRT

<213> Ehrlichia chaffeensis

<400> 10

Met Asn Cys Lys Lys Phe Phe Ile Thr Thr Ala Leu Val Ser Leu Met
1 5 10 15

Ser Phe Leu Pro Gly Ile Ser Phe Ser Asp Pro Val Gln Gly Asp Asn
20 25 30

Ile Ser Gly Asn Phe Tyr Val Ser Gly Lys Tyr Met Pro Ser Ala Ser
35 40 45

His Phe Gly Met Phe Ser Ala Lys Glu Glu Lys Asn Pro Thr Val Ala
50 55 60

Leu Tyr Gly Leu Lys Gln Asp Trp Glu Gly Ile Ser Ser Ser Ser His
65 70 75 80

Asn Asp Asn His Phe Asn Asn Lys Gly Tyr Ser Phe Lys Tyr Glu Asn
85 90 95

Asn Pro Phe Leu Gly Phe Ala Gly Ala Ile Gly Tyr Ser Met Gly Gly
100 105 110

Pro Arg Val Glu Phe Glu Val Ser Tyr Glu Thr Phe Asp Val Lys Asn
115 120 125

Gln Gly Asn Asn Tyr Lys Asn Asp Ala His Arg Tyr Cys Ala Leu Gly
130 135 140

Gln Gln Asp Asn Ser Gly Ile Pro Lys Thr Ser Lys Tyr Val Leu Leu
145 150 155 160

Lys Ser Glu Gly Leu Leu Asp Ile Ser Phe Met Leu Asn Ala Cys Tyr
165 170 175

Asp Ile Ile Asn Glu Ser Ile Pro Leu Ser Pro Tyr Ile Cys Ala Gly
180 185 190

Val Gly Thr Asp Leu Ile Ser Met Phe Glu Ala Thr Asn Pro Lys Ile
195 200 205

Ser Tyr Gln Gly Lys Leu Gly Leu Ser Tyr Ser Ile Asn Pro Glu Ala
 210 215 220

Ser Val Phe Ile Gly Gly His Phe His Lys Val Ile Gly Asn Glu Phe
 225 230 235 240

Arg Asp Ile Pro Thr Leu Lys Ala Phe Val Thr Ser Ser Ala Thr Pro
 245 250 255

Asp Leu Ala Ile Val Thr Leu Ser Val Cys His Phe Gly Ile Glu Leu
 260 265 270

Gly Gly Arg Phe Asn Phe
 275

<210> 11
 <211> 843
 <212> DNA
 <213> Ehrlichia chaffeensis

<220>
 <221> CDS
 <222> (1)..(843)

<400> 11

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 Met Asn Cys Lys Lys Phe Phe Ile Thr Thr Thr Leu Val Ser Leu Met
 1 5 10 15

tcc ttc tta cct gga ata tca ttt tct gat gca gta cag aac gac aat 96
 Ser Phe Leu Pro Gly Ile Ser Phe Ser Asp Ala Val Gln Asn Asp Asn
 20 25 30

gtt ggt ggt aat ttc tat atc agt ggg aaa tat gta cca agt gtt tca 144
 Val Gly Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Val Pro Ser Val Ser
 35 40 45

cat ttt ggc gta ttc tct gct aaa cag gaa aga aat aca aca acc gga 192
 His Phe Gly Val Phe Ser Ala Lys Gln Glu Arg Asn Thr Thr Thr Gly
 50 55 60

gta ttt gga tta aag caa gat tgg gat ggc agc aca ata tct aaa aat 240
 Val Phe Gly Leu Lys Gln Asp Trp Asp Gly Ser Thr Ile Ser Lys Asn
 65 70 75 80

tct cca gaa aat aca ttt aac gtt cca aat tat tca ttt aaa tat gaa 288

Ser	Pro	Glu	Asn	Thr	Phe	Asn	Val	Pro	Asn	Tyr	Ser	Phe	Lys	Tyr	Glu		
				85					90					95			
aat	aat	cca	ttt	cta	ggt	ttt	gca	gga	gct	ggt	ggt	tat	tta	atg	aat	336	
Asn	Asn	Pro	Phe	Leu	Gly	Phe	Ala	Gly	Ala	Val	Gly	Tyr	Leu	Met	Asn		
			100					105					110				
ggt	cca	aga	ata	gag	tta	gaa	atg	tcc	tat	gaa	aca	ttt	gat	gtg	aaa	384	
Gly	Pro	Arg	Ile	Glu	Leu	Glu	Met	Ser	Tyr	Glu	Thr	Phe	Asp	Val	Lys		
		115					120					125					
aac	cag	ggt	aat	aac	tat	aag	aac	gat	gct	cac	aaa	tat	tat	gct	tta	432	
Asn	Gln	Gly	Asn	Asn	Tyr	Lys	Asn	Asp	Ala	His	Lys	Tyr	Tyr	Ala	Leu		
		130				135					140						
acc	cat	aac	agt	ggg	gga	aag	cta	agc	aat	gca	ggt	gat	aag	ttt	ggt	480	
Thr	His	Asn	Ser	Gly	Gly	Lys	Leu	Ser	Asn	Ala	Gly	Asp	Lys	Phe	Val		
145					150					155					160		
ttt	cta	aaa	aat	gaa	gga	cta	ctt	gat	ata	tca	ctt	atg	ttg	aat	gca	528	
Phe	Leu	Lys	Asn	Glu	Gly	Leu	Leu	Asp	Ile	Ser	Leu	Met	Leu	Asn	Ala		
			165					170					175				
tgc	tat	gat	gta	ata	agt	gaa	gga	ata	cct	ttc	tct	cct	tac	ata	tgt	576	
Cys	Tyr	Asp	Val	Ile	Ser	Glu	Gly	Ile	Pro	Phe	Ser	Pro	Tyr	Ile	Cys		
			180					185					190				
gca	ggt	ggt	ggt	act	gat	tta	ata	tcc	atg	ttt	gaa	gct	ata	aac	cct	624	
Ala	Gly	Val	Gly	Thr	Asp	Leu	Ile	Ser	Met	Phe	Glu	Ala	Ile	Asn	Pro		
		195				200						205					
aaa	att	tct	tat	caa	gga	aag	tta	ggt	ttg	agt	tac	tcc	ata	agc	cca	672	
Lys	Ile	Ser	Tyr	Gln	Gly	Lys	Leu	Gly	Leu	Ser	Tyr	Ser	Ile	Ser	Pro		
	210					215					220						
gaa	gct	tct	ggt	ttt	ggt	gga	cat	ttt	cat	aag	gtg	ata	ggg	aat		720	
Glu	Ala	Ser	Val	Phe	Val	Gly	Gly	His	Phe	His	Lys	Val	Ile	Gly	Asn		
225				230				235				240					
gaa	ttc	aga	gat	att	cct	gct	atg	ata	ccc	agt	acc	tca	act	ctc	aca	768	
Glu	Phe	Arg	Asp	Ile	Pro	Ala	Met	Ile	Pro	Ser	Thr	Ser	Thr	Leu	Thr		
			245					250					255				
ggt	aat	cac	ttt	act	ata	gta	aca	cta	agt	gta	tgc	cac	ttt	gga	gtg	816	
Gly	Asn	His	Phe	Thr	Ile	Val	Thr	Leu	Ser	Val	Cys	His	Phe	Gly	Val		
		260						265					270				
gaa	ctt	gga	gga	agg	ttt	aac	ttt	taa								843	

Glu Leu Gly Gly Arg Phe Asn Phe
275 280

<210> 12

<211> 280

<212> PRT

<213> Ehrlichia chaffeensis

<400> 12

Met Asn Cys Lys Lys Phe Phe Ile Thr Thr Thr Leu Val Ser Leu Met
1 5 10 15

Ser Phe Leu Pro Gly Ile Ser Phe Ser Asp Ala Val Gln Asn Asp Asn
20 25 30

Val Gly Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Val Pro Ser Val Ser
35 40 45

His Phe Gly Val Phe Ser Ala Lys Gln Glu Arg Asn Thr Thr Thr Gly
50 55 60

Val Phe Gly Leu Lys Gln Asp Trp Asp Gly Ser Thr Ile Ser Lys Asn
65 70 75 80

Ser Pro Glu Asn Thr Phe Asn Val Pro Asn Tyr Ser Phe Lys Tyr Glu
85 90 95

Asn Asn Pro Phe Leu Gly Phe Ala Gly Ala Val Gly Tyr Leu Met Asn
100 105 110

Gly Pro Arg Ile Glu Leu Glu Met Ser Tyr Glu Thr Phe Asp Val Lys
115 120 125

Asn Gln Gly Asn Asn Tyr Lys Asn Asp Ala His Lys Tyr Tyr Ala Leu
130 135 140

Thr His Asn Ser Gly Gly Lys Leu Ser Asn Ala Gly Asp Lys Phe Val
145 150 155 160

Phe Leu Lys Asn Glu Gly Leu Leu Asp Ile Ser Leu Met Leu Asn Ala
165 170 175

Cys Tyr Asp Val Ile Ser Glu Gly Ile Pro Phe Ser Pro Tyr Ile Cys
180 185 190

Ala Gly Val Gly Thr Asp Leu Ile Ser Met Phe Glu Ala Ile Asn Pro
195 200 205

Lys Ile Ser Tyr Gln Gly Lys Leu Gly Leu Ser Tyr Ser Ile Ser Pro
 210 215 220

Glu Ala Ser Val Phe Val Gly Gly His Phe His Lys Val Ile Gly Asn
 225 230 235 240

Glu Phe Arg Asp Ile Pro Ala Met Ile Pro Ser Thr Ser Thr Leu Thr
 245 250 255

Gly Asn His Phe Thr Ile Val Thr Leu Ser Val Cys His Phe Gly Val
 260 265 270

Glu Leu Gly Gly Arg Phe Asn Phe
 275 280

<210> 13

<211> 894

<212> DNA

<213> Ehrlichia chaffeensis

<220>

<221> CDS

<222> (1)..(894)

<400> 13

atg gaa aat ctc atg aat aag aaa aac aaa ttc ttt aca ata agt aca 48
 Met Glu Asn Leu Met Asn Lys Lys Asn Lys Phe Phe Thr Ile Ser Thr
 1 5 10 15

gca atg gta tgc tta ttg tta tta cct ggt ata tca ttt tca gaa act 96
 Ala Met Val Cys Leu Leu Leu Leu Pro Gly Ile Ser Phe Ser Glu Thr
 20 25 30

ata aac aac agt gct aaa aaa cag cct ggg tta tat atc agt ggg cag 144
 Ile Asn Asn Ser Ala Lys Lys Gln Pro Gly Leu Tyr Ile Ser Gly Gln
 35 40 45

tac aaa cct agt gtt tca gtt ttt agt aat ttt tca gta aaa gaa act 192
 Tyr Lys Pro Ser Val Ser Val Phe Ser Asn Phe Ser Val Lys Glu Thr
 50 55 60

aat gtt ccc aca aag cag tta ata gca ctt aaa aaa gac att aat tct 240
 Asn Val Pro Thr Lys Gln Leu Ile Ala Leu Lys Lys Asp Ile Asn Ser
 65 70 75 80

gtt gca gtt ggt agt aat gct act aca ggt att agc aat cca ggt aat 288

Val	Ala	Val	Gly	Ser	Asn	Ala	Thr	Thr	Gly	Ile	Ser	Asn	Pro	Gly	Asn		
				85					90					95			
ttc	aca	att	cct	tat	act	gca	gaa	ttt	caa	gat	aat	gtt	gcc	aat	ttc	336	
Phe	Thr	Ile	Pro	Tyr	Thr	Ala	Glu	Phe	Gln	Asp	Asn	Val	Ala	Asn	Phe		
			100					105					110				
aat	ggg	gct	gtt	ggt	tac	tct	ttt	cct	gat	agt	cta	aga	att	gaa	ata	384	
Asn	Gly	Ala	Val	Gly	Tyr	Ser	Phe	Pro	Asp	Ser	Leu	Arg	Ile	Glu	Ile		
			115				120					125					
gag	gga	ttt	cat	gaa	aaa	ttt	gat	gtc	aaa	aac	cct	gga	ggt	tac	aca	432	
Glu	Gly	Phe	His	Glu	Lys	Phe	Asp	Val	Lys	Asn	Pro	Gly	Gly	Tyr	Thr		
			130			135					140						
caa	gta	aaa	gat	gcg	tac	cgt	tat	ttt	gca	cta	gca	cgt	gat	tta	aaa	480	
Gln	Val	Lys	Asp	Ala	Tyr	Arg	Tyr	Phe	Ala	Leu	Ala	Arg	Asp	Leu	Lys		
145					150					155					160		
gat	ggc	ttc	ttt	gaa	cct	aaa	gcg	gaa	gat	aca	ggg	gtt	tat	cat	act	528	
Asp	Gly	Phe	Phe	Glu	Pro	Lys	Ala	Glu	Asp	Thr	Gly	Val	Tyr	His	Thr		
				165					170					175			
gtt	atg	aaa	aat	gat	gga	tta	tct	att	tta	tct	act	atg	gtt	aac	gtc	576	
Val	Met	Lys	Asn	Asp	Gly	Leu	Ser	Ile	Leu	Ser	Thr	Met	Val	Asn	Val		
			180					185					190				
tgt	tac	gat	ttt	tct	gta	gat	gaa	tta	cca	gtc	tta	cct	tat	ata	tgt	624	
Cys	Tyr	Asp	Phe	Ser	Val	Asp	Glu	Leu	Pro	Val	Leu	Pro	Tyr	Ile	Cys		
			195				200					205					
gca	ggt	atg	ggt	ata	aac	gcc	ata	gaa	ttc	ttc	gac	gct	tta	cat	gta	672	
Ala	Gly	Met	Gly	Ile	Asn	Ala	Ile	Glu	Phe	Phe	Asp	Ala	Leu	His	Val		
			210			215					220						
aaa	ttt	gct	tac	caa	ggc	aaa	cta	ggt	att	agc	tat	caa	cta	ttt	act	720	
Lys	Phe	Ala	Tyr	Gln	Gly	Lys	Leu	Gly	Ile	Ser	Tyr	Gln	Leu	Phe	Thr		
225					230					235				240			
aaa	gta	aat	tta	ttc	ctt	gat	ggg	tat	tac	cat	caa	gta	ata	ggc	aat	768	
Lys	Val	Asn	Leu	Phe	Leu	Asp	Gly	Tyr	Tyr	His	Gln	Val	Ile	Gly	Asn		
				245				250					255				
caa	ttc	aaa	aac	tta	aac	gta	aac	cat	gtt	tac	aca	ctt	aaa	gaa	tct	816	
Gln	Phe	Lys	Asn	Leu	Asn	Val	Asn	His	Val	Tyr	Thr	Leu	Lys	Glu	Ser		
			260					265					270				
cct	aaa	gtc	aca	tct	gca	gta	gct	aca	ctt	gac	att	gca	tac	ttt	ggt	864	

Pro Lys Val Thr Ser Ala Val Ala Thr Leu Asp Ile Ala Tyr Phe Gly
 275 280 285

ggc gaa gtt gga ata aga ttc aca ttt taa
 Gly Glu Val Gly Ile Arg Phe Thr Phe
 290 295

894

<210> 14
 <211> 297
 <212> PRT
 <213> Ehrlichia chaffeensis

<400> 14
 Met Glu Asn Leu Met Asn Lys Lys Asn Lys Phe Phe Thr Ile Ser Thr
 1 5 10 15

Ala Met Val Cys Leu Leu Leu Leu Pro Gly Ile Ser Phe Ser Glu Thr
 20 25 30

Ile Asn Asn Ser Ala Lys Lys Gln Pro Gly Leu Tyr Ile Ser Gly Gln
 35 40 45

Tyr Lys Pro Ser Val Ser Val Phe Ser Asn Phe Ser Val Lys Glu Thr
 50 55 60

Asn Val Pro Thr Lys Gln Leu Ile Ala Leu Lys Lys Asp Ile Asn Ser
 65 70 75 80

Val Ala Val Gly Ser Asn Ala Thr Thr Gly Ile Ser Asn Pro Gly Asn
 85 90 95

Phe Thr Ile Pro Tyr Thr Ala Glu Phe Gln Asp Asn Val Ala Asn Phe
 100 105 110

Asn Gly Ala Val Gly Tyr Ser Phe Pro Asp Ser Leu Arg Ile Glu Ile
 115 120 125

Glu Gly Phe His Glu Lys Phe Asp Val Lys Asn Pro Gly Gly Tyr Thr
 130 135 140

Gln Val Lys Asp Ala Tyr Arg Tyr Phe Ala Leu Ala Arg Asp Leu Lys
 145 150 155 160

Asp Gly Phe Phe Glu Pro Lys Ala Glu Asp Thr Gly Val Tyr His Thr
 165 170 175

Val Met Lys Asn Asp Gly Leu Ser Ile Leu Ser Thr Met Val Asn Val

180	185	190
Cys Tyr Asp Phe Ser Val Asp Glu Leu Pro Val Leu Pro Tyr Ile Cys		
195	200	205
Ala Gly Met Gly Ile Asn Ala Ile Glu Phe Phe Asp Ala Leu His Val		
210	215	220
Lys Phe Ala Tyr Gln Gly Lys Leu Gly Ile Ser Tyr Gln Leu Phe Thr		
225	230	235 240
Lys Val Asn Leu Phe Leu Asp Gly Tyr Tyr His Gln Val Ile Gly Asn		
	245	250 255
Gln Phe Lys Asn Leu Asn Val Asn His Val Tyr Thr Leu Lys Glu Ser		
	260	265 270
Pro Lys Val Thr Ser Ala Val Ala Thr Leu Asp Ile Ala Tyr Phe Gly		
	275	280 285
Gly Glu Val Gly Ile Arg Phe Thr Phe		
290	295	

<210> 15
 <211> 591
 <212> DNA
 <213> Ehrlichia chaffeensis

<220>
 <221> CDS
 <222> (1)..(591)

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 atg ata tat aaa gaa aaa ctt act aga gtg gga gaa tat atc tta gca 48
 Met Ile Tyr Lys Glu Lys Leu Thr Arg Val Gly Glu Tyr Ile Leu Ala
 1 5 10 15
 tat tta tca ttt att ctt tct act tat atc ttt cta gtg ctg gta aat 96
 Tyr Leu Ser Phe Ile Leu Ser Thr Tyr Ile Phe Leu Val Leu Val Asn
 20 25 30
 att att aga tat aac agc ctt gct ata tgt gtt atc agt cta cta aga 144
 Ile Ile Arg Tyr Asn Ser Leu Ala Ile Cys Val Ile Ser Leu Leu Arg
 35 40 45
 act aat atc ttt aac gtt agc aca aaa aaa tta ata aaa gat aaa tgt 192
 Thr Asn Ile Phe Asn Val Ser Thr Lys Lys Leu Ile Lys Asp Lys Cys

50

55

60

cgt gat act aag ttt agt aac atg aat tgt tat ttg tac ggt aaa ccg 240
 Arg Asp Thr Lys Phe Ser Asn Met Asn Cys Tyr Leu Tyr Gly Lys Pro
 65 70 75 80

tta aat tta caa att ttt tat gga ata ttt tcc ttt att aga aac ttt 288
 Leu Asn Leu Gln Ile Phe Tyr Gly Ile Phe Ser Phe Ile Arg Asn Phe
 85 90 95

caa aat aac aca cta ata att cct aat gat agt aaa tgc ggc ttc tat 336
 Gln Asn Asn Thr Leu Ile Ile Pro Asn Asp Ser Lys Cys Gly Phe Tyr
 100 105 110

acc acg tta tgg gat aat cca gca cta cat tat aca tat aca ctt act 384
 Thr Thr Leu Trp Asp Asn Pro Ala Leu His Tyr Thr Tyr Thr Leu Thr
 115 120 125

ggc agt gag tac cgt aat ttt ttt gac att cta tat gaa aac att atc 432
 Gly Ser Glu Tyr Arg Asn Phe Phe Asp Ile Leu Tyr Glu Asn Ile Ile
 130 135 140

tgt caa tgt aaa tta ctt att aac tat aac cgt tct gta tta aac caa 480
 Cys Gln Cys Lys Leu Leu Ile Asn Tyr Asn Arg Ser Val Leu Asn Gln
 145 150 155 160

cat aat aaa aat act ctc gta ata ata cca ata cct aat gct aga gag 528
 His Asn Lys Asn Thr Leu Val Ile Ile Pro Ile Pro Asn Ala Arg Glu
 165 170 175

ttc agt aat gaa att cga gta agg aat ata tca ata aat aag gaa agt 576
 Phe Ser Asn Glu Ile Arg Val Arg Asn Ile Ser Ile Asn Lys Glu Ser
 180 185 190

tct tat gag tgc taa 591
 Ser Tyr Glu Cys
 195

<210> 16

<211> 196

<212> PRT

<213> Ehrlichia chaffeensis

<400> 16

Met Ile Tyr Lys Glu Lys Leu Thr Arg Val Gly Glu Tyr Ile Leu Ala
 1 5 10 15

Tyr Leu Ser Phe Ile Leu Ser Thr Tyr Ile Phe Leu Val Leu Val Asn
 20 25 30

Ile Ile Arg Tyr Asn Ser Leu Ala Ile Cys Val Ile Ser Leu Leu Arg
 35 40 45

Thr Asn Ile Phe Asn Val Ser Thr Lys Lys Leu Ile Lys Asp Lys Cys
 50 55 60

Arg Asp Thr Lys Phe Ser Asn Met Asn Cys Tyr Leu Tyr Gly Lys Pro
 65 70 75 80

Leu Asn Leu Gln Ile Phe Tyr Gly Ile Phe Ser Phe Ile Arg Asn Phe
 85 90 95

Gln Asn Asn Thr Leu Ile Ile Pro Asn Asp Ser Lys Cys Gly Phe Tyr
 100 105 110

Thr Thr Leu Trp Asp Asn Pro Ala Leu His Tyr Thr Tyr Thr Leu Thr
 115 120 125

Gly Ser Glu Tyr Arg Asn Phe Phe Asp Ile Leu Tyr Glu Asn Ile Ile
 130 135 140

Cys Gln Cys Lys Leu Leu Ile Asn Tyr Asn Arg Ser Val Leu Asn Gln
 145 150 155 160

His Asn Lys Asn Thr Leu Val Ile Ile Pro Ile Pro Asn Ala Arg Glu
 165 170 175

Phe Ser Asn Glu Ile Arg Val Arg Asn Ile Ser Ile Asn Lys Glu Ser
 180 185 190

Ser Tyr Glu Cys
 195

<210> 17

<211> 876

<212> DNA

<213> Ehrlichia chaffeensis

<220>

<221> CDS

<222> (1)..(876)

<400> 17

atg aat aaa aaa aac aag ttt att ata gct aca gca ttg gta tat tta 48

Met	Asn	Lys	Lys	Asn	Lys	Phe	Ile	Ile	Ala	Thr	Ala	Leu	Val	Tyr	Leu	
1				5					10					15		
ctg	tca	tta	cct	agt	gta	tcg	ttt	tca	gag	gtt	aca	aac	agc	agt	att	96
Leu	Ser	Leu	Pro	Ser	Val	Ser	Phe	Ser	Glu	Val	Thr	Asn	Ser	Ser	Ile	
			20					25					30			
aaa	aaa	cac	tct	ggg	tta	tat	att	agt	gga	caa	tac	aaa	cca	agt	gtt	144
Lys	Lys	His	Ser	Gly	Leu	Tyr	Ile	Ser	Gly	Gln	Tyr	Lys	Pro	Ser	Val	
		35					40						45			
tct	gtt	ttt	agt	agt	ttc	tca	att	aaa	gaa	act	aac	act	atc	aca	aaa	192
Ser	Val	Phe	Ser	Ser	Phe	Ser	Ile	Lys	Glu	Thr	Asn	Thr	Ile	Thr	Lys	
	50					55					60					
aat	ctt	ata	gcg	tta	aaa	aaa	gat	att	aac	tct	ctt	gaa	gtt	aac	gcc	240
Asn	Leu	Ile	Ala	Leu	Lys	Lys	Asp	Ile	Asn	Ser	Leu	Glu	Val	Asn	Ala	
65					70					75					80	
gat	gct	agt	caa	ggg	att	agt	cat	cca	gga	aat	ttt	act	ata	cct	tat	288
Asp	Ala	Ser	Gln	Gly	Ile	Ser	His	Pro	Gly	Asn	Phe	Thr	Ile	Pro	Tyr	
			85					90						95		
ata	gca	gca	ttt	gaa	gat	aat	gct	ttt	aat	ttc	aac	ggg	gct	att	ggg	336
Ile	Ala	Ala	Phe	Glu	Asp	Asn	Ala	Phe	Asn	Phe	Asn	Gly	Ala	Ile	Gly	
			100					105					110			
tac	att	act	gaa	ggg	cta	agg	att	gaa	ata	gaa	ggg	tcc	tat	gaa	gaa	384
Tyr	Ile	Thr	Glu	Gly	Leu	Arg	Ile	Glu	Ile	Glu	Gly	Ser	Tyr	Glu	Glu	
		115					120					125				
ttt	gat	gct	aaa	aac	cct	gga	ggg	tat	ggg	cta	aat	gat	gcc	ttt	cgg	432
Phe	Asp	Ala	Lys	Asn	Pro	Gly	Gly	Tyr	Gly	Leu	Asn	Asp	Ala	Phe	Arg	
	130					135					140					
tac	ttt	gct	tta	gca	cgt	gat	atg	gaa	agc	aac	aag	ttc	caa	cca	aaa	480
Tyr	Phe	Ala	Leu	Ala	Arg	Asp	Met	Glu	Ser	Asn	Lys	Phe	Gln	Pro	Lys	
145					150					155					160	
gca	caa	agc	tca	caa	aaa	gta	ttt	cac	act	gta	atg	aag	agt	gat	ggg	528
Ala	Gln	Ser	Ser	Gln	Lys	Val	Phe	His	Thr	Val	Met	Lys	Ser	Asp	Gly	
				165					170					175		
tta	tct	ata	ata	tct	atc	atg	gtt	aac	ggc	tgt	tat	gat	ttt	tct	tcg	576
Leu	Ser	Ile	Ile	Ser	Ile	Met	Val	Asn	Gly	Cys	Tyr	Asp	Phe	Ser	Ser	
			180					185					190			
gat	aat	tta	tta	gta	tca	cct	tat	ata	tgt	gga	ggg	ata	ggg	gtg	gat	624

Asp Asn Leu Leu Val Ser Pro Tyr Ile Cys Gly Gly Ile Gly Val Asp
 195 200 205

gca ata gaa ttt ttt gac gca tta cac att aaa ctt gcg tgc caa agc 672
 Ala Ile Glu Phe Phe Asp Ala Leu His Ile Lys Leu Ala Cys Gln Ser
 210 215 220

aaa tta ggc atc act tat caa tta tct tat aat atc agc tta ttt gct 720
 Lys Leu Gly Ile Thr Tyr Gln Leu Ser Tyr Asn Ile Ser Leu Phe Ala
 225 230 235 240

gat gga tat tat cat caa gta ata ggt aac caa ttc aga aat tta aac 768
 Asp Gly Tyr Tyr His Gln Val Ile Gly Asn Gln Phe Arg Asn Leu Asn
 245 250 255

gtt caa cat gta gct gaa ctt aat gat gca cct aaa gtt aca tct gca 816
 Val Gln His Val Ala Glu Leu Asn Asp Ala Pro Lys Val Thr Ser Ala
 260 265 270

gtt gcc aca ctt aat gtt gga tat ttc ggc gct gaa gtt gga gta aga 864
 Val Ala Thr Leu Asn Val Gly Tyr Phe Gly Ala Glu Val Gly Val Arg
 275 280 285

ttt ata ttt taa 876
 Phe Ile Phe
 290

<210> 18

<211> 291

<212> PRT

<213> Ehrlichia chaffeensis

<400> 18

Met Asn Lys Lys Asn Lys Phe Ile Ile Ala Thr Ala Leu Val Tyr Leu
 1 5 10 15

Leu Ser Leu Pro Ser Val Ser Phe Ser Glu Val Thr Asn Ser Ser Ile
 20 25 30

Lys Lys His Ser Gly Leu Tyr Ile Ser Gly Gln Tyr Lys Pro Ser Val
 35 40 45

Ser Val Phe Ser Ser Phe Ser Ile Lys Glu Thr Asn Thr Ile Thr Lys
 50 55 60

Asn Leu Ile Ala Leu Lys Lys Asp Ile Asn Ser Leu Glu Val Asn Ala
 65 70 75 80

Asp Ala Ser Gln Gly Ile Ser His Pro Gly Asn Phe Thr Ile Pro Tyr
85 90 95

Ile Ala Ala Phe Glu Asp Asn Ala Phe Asn Phe Asn Gly Ala Ile Gly
100 105 110

Tyr Ile Thr Glu Gly Leu Arg Ile Glu Ile Glu Gly Ser Tyr Glu Glu
115 120 125

Phe Asp Ala Lys Asn Pro Gly Gly Tyr Gly Leu Asn Asp Ala Phe Arg
130 135 140

Tyr Phe Ala Leu Ala Arg Asp Met Glu Ser Asn Lys Phe Gln Pro Lys
145 150 155 160

Ala Gln Ser Ser Gln Lys Val Phe His Thr Val Met Lys Ser Asp Gly
165 170 175

Leu Ser Ile Ile Ser Ile Met Val Asn Gly Cys Tyr Asp Phe Ser Ser
180 185 190

Asp Asn Leu Leu Val Ser Pro Tyr Ile Cys Gly Gly Ile Gly Val Asp
195 200 205

Ala Ile Glu Phe Phe Asp Ala Leu His Ile Lys Leu Ala Cys Gln Ser
210 215 220

Lys Leu Gly Ile Thr Tyr Gln Leu Ser Tyr Asn Ile Ser Leu Phe Ala
225 230 235 240

Asp Gly Tyr Tyr His Gln Val Ile Gly Asn Gln Phe Arg Asn Leu Asn
245 250 255

Val Gln His Val Ala Glu Leu Asn Asp Ala Pro Lys Val Thr Ser Ala
260 265 270

Val Ala Thr Leu Asn Val Gly Tyr Phe Gly Ala Glu Val Gly Val Arg
275 280 285

Phe Ile Phe
290

<210> 19

<211> 396

<212> DNA

<213> Ehrlichia chaffeensis

<220>

<221> CDS

<222> (1)..(396)

<400> 19

tct aga ata cat gat gaa aat tat gct att aca aca aat aat aaa tta 48
Ser Arg Ile His Asp Glu Asn Tyr Ala Ile Thr Thr Asn Asn Lys Leu
1 5 10 15

tcc atc gca tct att atg gtt aac acc tgc tat gat att tca att aat 96
Ser Ile Ala Ser Ile Met Val Asn Thr Cys Tyr Asp Ile Ser Ile Asn
20 25 30

aat aca tca ata gta ccg tat tta tgc aca ggc att ggt gaa gat ctt 144
Asn Thr Ser Ile Val Pro Tyr Leu Cys Thr Gly Ile Gly Glu Asp Leu
35 40 45

gta ggg ctt ttt aat aca ata cat ttt aaa ctt gca tat caa ggg aaa 192
Val Gly Leu Phe Asn Thr Ile His Phe Lys Leu Ala Tyr Gln Gly Lys
50 55 60

gtt gga atg agt tat ttg ata aat aac aat atc cta tta ttt tct gac 240
Val Gly Met Ser Tyr Leu Ile Asn Asn Asn Ile Leu Leu Phe Ser Asp
65 70 75 80

ata tat tat cat aaa gtc atg ggt aac aga ttt aaa aat ttg tac atg 288
Ile Tyr Tyr His Lys Val Met Gly Asn Arg Phe Lys Asn Leu Tyr Met
85 90 95

caa tat gta gct gat cct aat att tct gaa gaa act ata cct ata tta 336
Gln Tyr Val Ala Asp Pro Asn Ile Ser Glu Glu Thr Ile Pro Ile Leu
100 105 110

gca aaa ctt gat att ggt tat ttt gga agt gaa att gga ata agg ttt 384
Ala Lys Leu Asp Ile Gly Tyr Phe Gly Ser Glu Ile Gly Ile Arg Phe
115 120 125

atg ttt aac taa 396
Met Phe Asn
130

<210> 20

<211> 131

<212> PRT

<213> Ehrlichia chaffeensis

<400> 20

Ser Arg Ile His Asp Glu Asn Tyr Ala Ile Thr Thr Asn Asn Lys Leu
1 5 10 15

Ser Ile Ala Ser Ile Met Val Asn Thr Cys Tyr Asp Ile Ser Ile Asn
20 25 30

Asn Thr Ser Ile Val Pro Tyr Leu Cys Thr Gly Ile Gly Glu Asp Leu
35 40 45

Val Gly Leu Phe Asn Thr Ile His Phe Lys Leu Ala Tyr Gln Gly Lys
50 55 60

Val Gly Met Ser Tyr Leu Ile Asn Asn Asn Ile Leu Leu Phe Ser Asp
65 70 75 80

Ile Tyr Tyr His Lys Val Met Gly Asn Arg Phe Lys Asn Leu Tyr Met
85 90 95

Gln Tyr Val Ala Asp Pro Asn Ile Ser Glu Glu Thr Ile Pro Ile Leu
100 105 110

Ala Lys Leu Asp Ile Gly Tyr Phe Gly Ser Glu Ile Gly Ile Arg Phe
115 120 125

Met Phe Asn
130

<210> 21

<211> 888

<212> DNA

<213> Ehrlichia chaffeensis

<220>

<221> CDS

<222> (1)..(888)

<400> 21

atg aca aag aaa ttt aat ttt gta aat gtt ata tta aca ttt ttg tta 48
Met Thr Lys Lys Phe Asn Phe Val Asn Val Ile Leu Thr Phe Leu Leu
1 5 10 15

ttt ctt ttc cca ctt aag tca ttt aca aca tat gca aat aat aac aca 96
Phe Leu Phe Pro Leu Lys Ser Phe Thr Thr Tyr Ala Asn Asn Asn Thr
20 25 30

atc act caa aaa gtt gga ttg tac ata agt ggt caa tat aag cca agt 144

Ile Thr Gln Lys Val Gly Leu Tyr Ile Ser Gly Gln Tyr Lys Pro Ser	
35 40 45	
att cct cat ttc aag aat ttt tca gta gaa gaa aat gac aaa gta gta	192
Ile Pro His Phe Lys Asn Phe Ser Val Glu Glu Asn Asp Lys Val Val	
50 55 60	
gat ttg ata ggt ctt aca act gat gtt aca tat atc aca gaa cat ata	240
Asp Leu Ile Gly Leu Thr Thr Asp Val Thr Tyr Ile Thr Glu His Ile	
65 70 75 80	
tta cga gat aat aca aaa ttc aac act cat tat att gca aag ttc aag	288
Leu Arg Asp Asn Thr Lys Phe Asn Thr His Tyr Ile Ala Lys Phe Lys	
85 90 95	
aac aat ttt ata aat ttc agc agt gca att ggt tat tat tct ggg caa	336
Asn Asn Phe Ile Asn Phe Ser Ser Ala Ile Gly Tyr Tyr Ser Gly Gln	
100 105 110	
gga cca agg tta gaa ata gaa agc tct tat ggg gat ttt gat gtt gta	384
Gly Pro Arg Leu Glu Ile Glu Ser Ser Tyr Gly Asp Phe Asp Val Val	
115 120 125	
aat tat aaa aat tat gca gta caa gat gtt aat aga tat ttt gct tta	432
Asn Tyr Lys Asn Tyr Ala Val Gln Asp Val Asn Arg Tyr Phe Ala Leu	
130 135 140	
gta cgt gaa aaa aat ggt tca aat ttc tct cca aaa cca cat gaa act	480
Val Arg Glu Lys Asn Gly Ser Asn Phe Ser Pro Lys Pro His Glu Thr	
145 150 155 160	
agt caa ccc tct gac agt aat cct aaa aag tct ttt tat act tta atg	528
Ser Gln Pro Ser Asp Ser Asn Pro Lys Lys Ser Phe Tyr Thr Leu Met	
165 170 175	
aag aat aat ggg gta ttt gtt gca tca gta ata atc aac ggt tgt tat	576
Lys Asn Asn Gly Val Phe Val Ala Ser Val Ile Ile Asn Gly Cys Tyr	
180 185 190	
gat ttt tct ttt aat aac aca aca ata tca cct tac gta tgt ata gga	624
Asp Phe Ser Phe Asn Asn Thr Thr Ile Ser Pro Tyr Val Cys Ile Gly	
195 200 205	
gtt gga gga gat ttt ata gag ttt ttt gaa gta atg cat atc aag ttt	672
Val Gly Gly Asp Phe Ile Glu Phe Phe Glu Val Met His Ile Lys Phe	
210 215 220	
gct tgc caa agt aag gtt ggt att agc tat cca ata tct ccc tct att	720

Ala Cys Gln Ser Lys Val Gly Ile Ser Tyr Pro Ile Ser Pro Ser Ile
 225 230 235 240

act att ttt gct gat gca vat tat cac aag gtc ata aat aat aaa ttt 768
 Thr Ile Phe Ala Asp Ala Xaa Tyr His Lys Val Ile Asn Asn Lys Phe
 245 250 255

aac aac cta cat gtt aag tat tca tat gaa ctt aaa aac tca cct acc 816
 Asn Asn Leu His Val Lys Tyr Ser Tyr Glu Leu Lys Asn Ser Pro Thr
 260 265 270

att acc tct gca aca gcc aaa cta aac att gaa tat ttt ggt ggt gaa 864
 Ile Thr Ser Ala Thr Ala Lys Leu Asn Ile Glu Tyr Phe Gly Gly Glu
 275 280 285

gtt ggg atg aga ttt ata ttt taa 888
 Val Gly Met Arg Phe Ile Phe
 290 295

<210> 22

<211> 295

<212> PRT

<213> Ehrlichia chaffeensis

<400> 22

Met Thr Lys Lys Phe Asn Phe Val Asn Val Ile Leu Thr Phe Leu Leu
 1 5 10 15

Phe Leu Phe Pro Leu Lys Ser Phe Thr Thr Tyr Ala Asn Asn Asn Thr
 20 25 30

Ile Thr Gln Lys Val Gly Leu Tyr Ile Ser Gly Gln Tyr Lys Pro Ser
 35 40 45

Ile Pro His Phe Lys Asn Phe Ser Val Glu Glu Asn Asp Lys Val Val
 50 55 60

Asp Leu Ile Gly Leu Thr Thr Asp Val Thr Tyr Ile Thr Glu His Ile
 65 70 75 80

Leu Arg Asp Asn Thr Lys Phe Asn Thr His Tyr Ile Ala Lys Phe Lys
 85 90 95

Asn Asn Phe Ile Asn Phe Ser Ser Ala Ile Gly Tyr Tyr Ser Gly Gln
 100 105 110

Gly Pro Arg Leu Glu Ile Glu Ser Ser Tyr Gly Asp Phe Asp Val Val

115	120	125
Asn Tyr Lys Asn Tyr Ala Val Gln Asp Val Asn Arg Tyr Phe Ala Leu		
130	135	140
Val Arg Glu Lys Asn Gly Ser Asn Phe Ser Pro Lys Pro His Glu Thr		
145	150	155
Ser Gln Pro Ser Asp Ser Asn Pro Lys Lys Ser Phe Tyr Thr Leu Met		
165	170	175
Lys Asn Asn Gly Val Phe Val Ala Ser Val Ile Ile Asn Gly Cys Tyr		
180	185	190
Asp Phe Ser Phe Asn Asn Thr Thr Ile Ser Pro Tyr Val Cys Ile Gly		
195	200	205
Val Gly Gly Asp Phe Ile Glu Phe Phe Glu Val Met His Ile Lys Phe		
210	215	220
Ala Cys Gln Ser Lys Val Gly Ile Ser Tyr Pro Ile Ser Pro Ser Ile		
225	230	235
Thr Ile Phe Ala Asp Ala Xaa Tyr His Lys Val Ile Asn Asn Lys Phe		
245	250	255
Asn Asn Leu His Val Lys Tyr Ser Tyr Glu Leu Lys Asn Ser Pro Thr		
260	265	270
Ile Thr Ser Ala Thr Ala Lys Leu Asn Ile Glu Tyr Phe Gly Gly Glu		
275	280	285
Val Gly Met Arg Phe Ile Phe		
290	295	

<210> 23

<211> 840

<212> DNA

<213> Ehrlichia chaffeensis

<220>

<221> CDS

<222> (1)..(840)

<400> 23

atg agc aaa aaa aag ttt att aca ata gga aca gta ctt gca tct cta 48
Met Ser Lys Lys Lys Phe Ile Thr Ile Gly Thr Val Leu Ala Ser Leu

1	5	10	15	
tta tca ttc tta tct att gaa tcc ttt tca gct ata aat cat aat cat	96			
Leu Ser Phe Leu Ser Ile Glu Ser Phe Ser Ala Ile Asn His Asn His				
20	25	30		
aca gga aat aac act agt ggt ata tat att aca ggg cag tat aga cca	144			
Thr Gly Asn Asn Thr Ser Gly Ile Tyr Ile Thr Gly Gln Tyr Arg Pro				
35	40	45		
gga gta tcc cat ttt agc aat ttc tca gta aaa gaa act aat gtt gat	192			
Gly Val Ser His Phe Ser Asn Phe Ser Val Lys Glu Thr Asn Val Asp				
50	55	60		
aca ata caa cta gta gga tat aaa aaa agt gcg tct tct atc gat cct	240			
Thr Ile Gln Leu Val Gly Tyr Lys Lys Ser Ala Ser Ser Ile Asp Pro				
65	70	75	80	
aac act tat tca aac ttt caa ggt cca tat act gtt aca ttt caa gat	288			
Asn Thr Tyr Ser Asn Phe Gln Gly Pro Tyr Thr Val Thr Phe Gln Asp				
85	90	95		
aat gct gct agt ttc agt gga gca att gga tat tct tac ccc gaa agt	336			
Asn Ala Ala Ser Phe Ser Gly Ala Ile Gly Tyr Ser Tyr Pro Glu Ser				
100	105	110		
cta aga ctt gaa ctt gaa ggt tct tac gaa aaa ttt gat gtc aaa gat	384			
Leu Arg Leu Glu Leu Glu Gly Ser Tyr Glu Lys Phe Asp Val Lys Asp				
115	120	125		
cct aaa gac tac tca gca aaa gat gct ttt agg ttt ttt gct cta gca	432			
Pro Lys Asp Tyr Ser Ala Lys Asp Ala Phe Arg Phe Phe Ala Leu Ala				
130	135	140		
cgt aat acg tct act act gtt cct gat gct caa aaa tat aca gtt atg	480			
Arg Asn Thr Ser Thr Thr Val Pro Asp Ala Gln Lys Tyr Thr Val Met				
145	150	155	160	
aag aat aat ggc tta tct gtt gca tca atc atg atc aat ggt tgt tat	528			
Lys Asn Asn Gly Leu Ser Val Ala Ser Ile Met Ile Asn Gly Cys Tyr				
165	170	175		
gat cta tct ttt aat aat tta gtc gta tca cct tat ata tgt gca ggt	576			
Asp Leu Ser Phe Asn Asn Leu Val Val Ser Pro Tyr Ile Cys Ala Gly				
180	185	190		
att ggt gaa gat ttc att gaa ttt ttt gat act ttg cac att aaa ctt	624			
Ile Gly Glu Asp Phe Ile Glu Phe Phe Asp Thr Leu His Ile Lys Leu				

195

200

205

gct tat caa gga aaa cta ggt att agt tat tac ttc ttt cct aag att 672
 Ala Tyr Gln Gly Lys Leu Gly Ile Ser Tyr Tyr Phe Phe Pro Lys Ile
 210 215 220

aat gta ttt gct ggt ggg tac tat cat aga gtt ata ggg aat aaa ttt 720
 Asn Val Phe Ala Gly Gly Tyr Tyr His Arg Val Ile Gly Asn Lys Phe
 225 230 235 240

aaa aat tta aat gtt aac cat gtt gtt aca ctt gat gaa ttt cct aaa 768
 Lys Asn Leu Asn Val Asn His Val Val Thr Leu Asp Glu Phe Pro Lys
 245 250 255

gca act tct gca gta gct aca ctt aat gtt gct tat ttt ggt ggt gaa 816
 Ala Thr Ser Ala Val Ala Thr Leu Asn Val Ala Tyr Phe Gly Gly Glu
 260 265 270

gct gga gta aag ttt aca ttt taa 840
 Ala Gly Val Lys Phe Thr Phe
 275 280

<210> 24

<211> 279

<212> PRT

<213> Ehrlichia chaffeensis

<400> 24

Met Ser Lys Lys Lys Phe Ile Thr Ile Gly Thr Val Leu Ala Ser Leu
 1 5 10 15

Leu Ser Phe Leu Ser Ile Glu Ser Phe Ser Ala Ile Asn His Asn His
 20 25 30

Thr Gly Asn Asn Thr Ser Gly Ile Tyr Ile Thr Gly Gln Tyr Arg Pro
 35 40 45

Gly Val Ser His Phe Ser Asn Phe Ser Val Lys Glu Thr Asn Val Asp
 50 55 60

Thr Ile Gln Leu Val Gly Tyr Lys Lys Ser Ala Ser Ser Ile Asp Pro
 65 70 75 80

Asn Thr Tyr Ser Asn Phe Gln Gly Pro Tyr Thr Val Thr Phe Gln Asp
 85 90 95

Asn Ala Ala Ser Phe Ser Gly Ala Ile Gly Tyr Ser Tyr Pro Glu Ser

100	105	110
Leu Arg Leu Glu Leu Glu Gly Ser Tyr Glu Lys Phe Asp Val Lys Asp		
115	120	125
Pro Lys Asp Tyr Ser Ala Lys Asp Ala Phe Arg Phe Phe Ala Leu Ala		
130	135	140
Arg Asn Thr Ser Thr Thr Val Pro Asp Ala Gln Lys Tyr Thr Val Met		
145	150	155 160
Lys Asn Asn Gly Leu Ser Val Ala Ser Ile Met Ile Asn Gly Cys Tyr		
165	170	175
Asp Leu Ser Phe Asn Asn Leu Val Val Ser Pro Tyr Ile Cys Ala Gly		
180	185	190
Ile Gly Glu Asp Phe Ile Glu Phe Phe Asp Thr Leu His Ile Lys Leu		
195	200	205
Ala Tyr Gln Gly Lys Leu Gly Ile Ser Tyr Tyr Phe Phe Pro Lys Ile		
210	215	220
Asn Val Phe Ala Gly Gly Tyr Tyr His Arg Val Ile Gly Asn Lys Phe		
225	230	235 240
Lys Asn Leu Asn Val Asn His Val Val Thr Leu Asp Glu Phe Pro Lys		
245	250	255
Ala Thr Ser Ala Val Ala Thr Leu Asn Val Ala Tyr Phe Gly Gly Glu		
260	265	270
Ala Gly Val Lys Phe Thr Phe		
275		

<210> 25
 <211> 852
 <212> DNA
 <213> Ehrlichia chaffeensis

<220>
 <221> CDS
 <222> (1)..(852)

<400> 25
 atg agt gct aaa aaa aag ctt ttt ata ata ggg tca gtg tta gta tgt 48
 Met Ser Ala Lys Lys Lys Leu Phe Ile Ile Gly Ser Val Leu Val Cys

1	5	10	15	
tta gtg tca tac tta cct act aaa tct ttg tca aac tta aat aat att	96			
Leu Val Ser Tyr Leu Pro Thr Lys Ser Leu Ser Asn Leu Asn Asn Ile				
20	25	30		
aat aat aac act aag tgc act ggg cta tat gtc agt gga caa tat aaa	144			
Asn Asn Asn Thr Lys Cys Thr Gly Leu Tyr Val Ser Gly Gln Tyr Lys				
35	40	45		
cct act gtt tct cac ttt agt aat ttt tca ctt aaa gaa act tat act	192			
Pro Thr Val Ser His Phe Ser Asn Phe Ser Leu Lys Glu Thr Tyr Thr				
50	55	60		
gac act aaa gag tta tta gga cta gca aaa gat att aag tct att aca	240			
Asp Thr Lys Glu Leu Leu Gly Leu Ala Lys Asp Ile Lys Ser Ile Thr				
65	70	75	80	
gat ata aca aca aat aaa aaa ttc aac att cct tat aac aca aaa ttt	288			
Asp Ile Thr Thr Asn Lys Lys Phe Asn Ile Pro Tyr Asn Thr Lys Phe				
85	90	95		
caa gat aat gct gtt agc ttc agt gca gct gtt gga tat att tcc caa	336			
Gln Asp Asn Ala Val Ser Phe Ser Ala Ala Val Gly Tyr Ile Ser Gln				
100	105	110		
gac agt cca agg gtt gag gta gaa tgg tct tat gaa gaa ttt gac gtt	384			
Asp Ser Pro Arg Val Glu Val Glu Trp Ser Tyr Glu Glu Phe Asp Val				
115	120	125		
aaa aat cct ggt aat tac gta gta agt gaa gcc ttc agg tat att gct	432			
Lys Asn Pro Gly Asn Tyr Val Val Ser Glu Ala Phe Arg Tyr Ile Ala				
130	135	140		
tta gca aga gga att gat aat ctt caa aaa tat cct gaa aca aat aag	480			
Leu Ala Arg Gly Ile Asp Asn Leu Gln Lys Tyr Pro Glu Thr Asn Lys				
145	150	155	160	
tat gtt gtt ata aag aac aat ggc tta tct gtc gca tcc att ata atc	528			
Tyr Val Val Ile Lys Asn Asn Gly Leu Ser Val Ala Ser Ile Ile Ile				
165	170	175		
aat ggc tgt tat gat ttt tct tta aac aat tta aaa gta tca cct tac	576			
Asn Gly Cys Tyr Asp Phe Ser Leu Asn Asn Leu Lys Val Ser Pro Tyr				
180	185	190		
ata tgc gta ggg ttt ggt ggg gac att ata gaa ttt ttt agt gct gta	624			
Ile Cys Val Gly Phe Gly Gly Asp Ile Ile Glu Phe Phe Ser Ala Val				

195

200

205

agt ttt aaa ttt gct tat caa ggt aag gta ggt atc agt tat cca tta 672
 Ser Phe Lys Phe Ala Tyr Gln Gly Lys Val Gly Ile Ser Tyr Pro Leu
 210 215 220

ttc tct aat atg att ata ttt gct gac gga tat tac cat aag gtc ata 720
 Phe Ser Asn Met Ile Ile Phe Ala Asp Gly Tyr Tyr His Lys Val Ile
 225 230 235 240

gga aat aaa ttt aac aat tta aat gtt caa cac gtt gtt agt ctt aac 768
 Gly Asn Lys Phe Asn Asn Leu Asn Val Gln His Val Val Ser Leu Asn
 245 250 255

agt cat cct aag tct act ttt gca gta gct act ctt aat gtt gag tat 816
 Ser His Pro Lys Ser Thr Phe Ala Val Ala Thr Leu Asn Val Glu Tyr
 260 265 270

ttc ggt agt gaa ttt ggg tta aaa ttt ata ttt taa 852
 Phe Gly Ser Glu Phe Gly Leu Lys Phe Ile Phe
 275 280

<210> 26

<211> 283

<212> PRT

<213> Ehrlichia chaffeensis

<400> 26

Met Ser Ala Lys Lys Lys Leu Phe Ile Ile Gly Ser Val Leu Val Cys
 1 5 10 15

Leu Val Ser Tyr Leu Pro Thr Lys Ser Leu Ser Asn Leu Asn Asn Ile
 20 25 30

Asn Asn Asn Thr Lys Cys Thr Gly Leu Tyr Val Ser Gly Gln Tyr Lys
 35 40 45

Pro Thr Val Ser His Phe Ser Asn Phe Ser Leu Lys Glu Thr Tyr Thr
 50 55 60

Asp Thr Lys Glu Leu Leu Gly Leu Ala Lys Asp Ile Lys Ser Ile Thr
 65 70 75 80

Asp Ile Thr Thr Asn Lys Lys Phe Asn Ile Pro Tyr Asn Thr Lys Phe
 85 90 95

Gln Asp Asn Ala Val Ser Phe Ser Ala Ala Val Gly Tyr Ile Ser Gln

100	105	110
Asp Ser Pro Arg Val Glu Val Glu Trp Ser Tyr Glu Glu Phe Asp Val		
115	120	125
Lys Asn Pro Gly Asn Tyr Val Val Ser Glu Ala Phe Arg Tyr Ile Ala		
130	135	140
Leu Ala Arg Gly Ile Asp Asn Leu Gln Lys Tyr Pro Glu Thr Asn Lys		
145	150	155
Tyr Val Val Ile Lys Asn Asn Gly Leu Ser Val Ala Ser Ile Ile Ile		
165	170	175
Asn Gly Cys Tyr Asp Phe Ser Leu Asn Asn Leu Lys Val Ser Pro Tyr		
180	185	190
Ile Cys Val Gly Phe Gly Gly Asp Ile Ile Glu Phe Phe Ser Ala Val		
195	200	205
Ser Phe Lys Phe Ala Tyr Gln Gly Lys Val Gly Ile Ser Tyr Pro Leu		
210	215	220
Phe Ser Asn Met Ile Ile Phe Ala Asp Gly Tyr Tyr His Lys Val Ile		
225	230	235
Gly Asn Lys Phe Asn Asn Leu Asn Val Gln His Val Val Ser Leu Asn		
245	250	255
Ser His Pro Lys Ser Thr Phe Ala Val Ala Thr Leu Asn Val Glu Tyr		
260	265	270
Phe Gly Ser Glu Phe Gly Leu Lys Phe Ile Phe		
275	280	

<210> 27

<211> 828

<212> DNA

<213> Ehrlichia chaffeensis

<220>

<221> CDS

<222> (1)..(828)

<400> 27

atg agt aaa aaa aat ttt att aca ata gga gca aca ctt att cat atg 48
Met Ser Lys Lys Asn Phe Ile Thr Ile Gly Ala Thr Leu Ile His Met

1	5	10	15	
ttg tta cct aac ata tct ttt cca gaa act att aac aat aac act gat	96			
Leu Leu Pro Asn Ile Ser Phe Pro Glu Thr Ile Asn Asn Asn Thr Asp				
20 25 30				
aaa ctt tct ggg tta tat ata agt ggg caa tat aaa cca ggg att tct	144			
Lys Leu Ser Gly Leu Tyr Ile Ser Gly Gln Tyr Lys Pro Gly Ile Ser				
35 40 45				
cat ttc agc aaa ttt tca gtc aaa gaa atc tat aat gat aac att caa	192			
His Phe Ser Lys Phe Ser Val Lys Glu Ile Tyr Asn Asp Asn Ile Gln				
50 55 60				
cta att ggg tta aga cac aac gca att tct act agt acc ctt aat att	240			
Leu Ile Gly Leu Arg His Asn Ala Ile Ser Thr Ser Thr Leu Asn Ile				
65 70 75 80				
aat aca gat ttt aat atc ccc tat aaa gta aca ttt caa aat aac att	288			
Asn Thr Asp Phe Asn Ile Pro Tyr Lys Val Thr Phe Gln Asn Asn Ile				
85 90 95				
acc agc ttt agt gga gct att ggt tat tct gat ccc aca ggg gca aga	336			
Thr Ser Phe Ser Gly Ala Ile Gly Tyr Ser Asp Pro Thr Gly Ala Arg				
100 105 110				
ttt gag ctt gaa ggt tct tat gaa gaa ttt gat gtg aca gat cct gga	384			
Phe Glu Leu Glu Gly Ser Tyr Glu Glu Phe Asp Val Thr Asp Pro Gly				
115 120 125				
gac tgc tta ata aaa gat acc tat aga tat ttc gct tta gct aga aac	432			
Asp Cys Leu Ile Lys Asp Thr Tyr Arg Tyr Phe Ala Leu Ala Arg Asn				
130 135 140				
cca tca ggt tct agc cct acc tca aac aac tat act gtt atg aga aat	480			
Pro Ser Gly Ser Ser Pro Thr Ser Asn Asn Tyr Thr Val Met Arg Asn				
145 150 155 160				
gat ggt gtt tcc att act tct gtt ata ttt aat ggc tgt tat gac atc	528			
Asp Gly Val Ser Ile Thr Ser Val Ile Phe Asn Gly Cys Tyr Asp Ile				
165 170 175				
ttt tta aag gat tta gaa gta tca cct tat gta tgt gtt ggt gta ggt	576			
Phe Leu Lys Asp Leu Glu Val Ser Pro Tyr Val Cys Val Gly Val Gly				
180 185 190				
gga gat ttt ata gaa ttt ttt gac gca tta cac att aaa tta gca tac	624			
Gly Asp Phe Ile Glu Phe Phe Asp Ala Leu His Ile Lys Leu Ala Tyr				

195 200 205

caa ggc aag tta ggt atc aat tat cac tta tcg act caa gca agc gta 672
 Gln Gly Lys Leu Gly Ile Asn Tyr His Leu Ser Thr Gln Ala Ser Val
 210 215 220

ttt att gat gga tat tat cat aag gtt ata gga aat caa ttc aac aat 720
 Phe Ile Asp Gly Tyr Tyr His Lys Val Ile Gly Asn Gln Phe Asn Asn
 225 230 235 240

cta aat gtt caa cac gtg gct agt aca gat ttt gga cct gta tac gca 768
 Leu Asn Val Gln His Val Ala Ser Thr Asp Phe Gly Pro Val Tyr Ala
 245 250 255

gta gcc aca ctt aac att ggt tat ttt ggt ggt gaa atc gga att aga 816
 Val Ala Thr Leu Asn Ile Gly Tyr Phe Gly Gly Glu Ile Gly Ile Arg
 260 265 270

ctt aca ttt taa 828
 Leu Thr Phe
 275

<210> 28
 <211> 275
 <212> PRT
 <213> Ehrlichia chaffeensis

<400> 28
 Met Ser Lys Lys Asn Phe Ile Thr Ile Gly Ala Thr Leu Ile His Met
 1 5 10 15

Leu Leu Pro Asn Ile Ser Phe Pro Glu Thr Ile Asn Asn Asn Thr Asp
 20 25 30

Lys Leu Ser Gly Leu Tyr Ile Ser Gly Gln Tyr Lys Pro Gly Ile Ser
 35 40 45

His Phe Ser Lys Phe Ser Val Lys Glu Ile Tyr Asn Asp Asn Ile Gln
 50 55 60

Leu Ile Gly Leu Arg His Asn Ala Ile Ser Thr Ser Thr Leu Asn Ile
 65 70 75 80

Asn Thr Asp Phe Asn Ile Pro Tyr Lys Val Thr Phe Gln Asn Asn Ile
 85 90 95

Thr Ser Phe Ser Gly Ala Ile Gly Tyr Ser Asp Pro Thr Gly Ala Arg

100	105	110
Phe Glu Leu Glu Gly Ser Tyr Glu Glu Phe Asp Val Thr Asp Pro Gly		
115	120	125
Asp Cys Leu Ile Lys Asp Thr Tyr Arg Tyr Phe Ala Leu Ala Arg Asn		
130	135	140
Pro Ser Gly Ser Ser Pro Thr Ser Asn Asn Tyr Thr Val Met Arg Asn		
145	150	155
Asp Gly Val Ser Ile Thr Ser Val Ile Phe Asn Gly Cys Tyr Asp Ile		
165	170	175
Phe Leu Lys Asp Leu Glu Val Ser Pro Tyr Val Cys Val Gly Val Gly		
180	185	190
Gly Asp Phe Ile Glu Phe Phe Asp Ala Leu His Ile Lys Leu Ala Tyr		
195	200	205
Gln Gly Lys Leu Gly Ile Asn Tyr His Leu Ser Thr Gln Ala Ser Val		
210	215	220
Phe Ile Asp Gly Tyr Tyr His Lys Val Ile Gly Asn Gln Phe Asn Asn		
225	230	235
Leu Asn Val Gln His Val Ala Ser Thr Asp Phe Gly Pro Val Tyr Ala		
245	250	255
Val Ala Thr Leu Asn Ile Gly Tyr Phe Gly Gly Glu Ile Gly Ile Arg		
260	265	270
Leu Thr Phe		
275		

<210> 29
 <211> 858
 <212> DNA
 <213> Ehrlichia chaffeensis

<220>
 <221> CDS
 <222> (1)..(858)

<400> 29
 atg aat aat aga aaa agt ttt ttt ata ata ggt gca tca tta cta gca 48
 Met Asn Asn Arg Lys Ser Phe Phe Ile Ile Gly Ala Ser Leu Leu Ala

1	5	10	15	
agc tta tta ttc aca tct gag gcc tct tct aca gga aat gta agt aac	96			
Ser Leu Leu Phe Thr Ser Glu Ala Ser Ser Thr Gly Asn Val Ser Asn				
20 25 30				
cat act tat ttt aaa cct agg tta tat atc agt gga caa tat aga cca	144			
His Thr Tyr Phe Lys Pro Arg Leu Tyr Ile Ser Gly Gln Tyr Arg Pro				
35 40 45				
gga gtt tct cat ttt agc aaa ttt tca gtc aaa gaa acc aac tac aat	192			
Gly Val Ser His Phe Ser Lys Phe Ser Val Lys Glu Thr Asn Tyr Asn				
50 55 60				
act act caa cta gtt ggg ctt aaa aag gac atc agt gtc ata ggg aac	240			
Thr Thr Gln Leu Val Gly Leu Lys Lys Asp Ile Ser Val Ile Gly Asn				
65 70 75 80				
agt aat atc aca acc tac aca aat ttc aac ttt cct tac att gca gaa	288			
Ser Asn Ile Thr Thr Tyr Thr Asn Phe Asn Phe Pro Tyr Ile Ala Glu				
85 90 95				
ttt caa gac aat gcc ata agt ttc agt ggg gca att gga tac ttg tat	336			
Phe Gln Asp Asn Ala Ile Ser Phe Ser Gly Ala Ile Gly Tyr Leu Tyr				
100 105 110				
tcc gag aat ttt aga att gaa gta gag gct tct tat gaa gaa ttt gat	384			
Ser Glu Asn Phe Arg Ile Glu Val Glu Ala Ser Tyr Glu Glu Phe Asp				
115 120 125				
ggt aaa aat cca gaa gga tct gct aca gac gca tac agg tat ttt gca	432			
Val Lys Asn Pro Glu Gly Ser Ala Thr Asp Ala Tyr Arg Tyr Phe Ala				
130 135 140				
cta gca cgt gct atg gat ggc act aat aaa tct agt cct gat gac aca	480			
Leu Ala Arg Ala Met Asp Gly Thr Asn Lys Ser Ser Pro Asp Asp Thr				
145 150 155 160				
aga aaa ttc act gtc atg aga aat gac ggg tta tca att tca tca gta	528			
Arg Lys Phe Thr Val Met Arg Asn Asp Gly Leu Ser Ile Ser Ser Val				
165 170 175				
atg ata aat ggg tgt tac aat ttt aca tta gat gat ata cca gta gta	576			
Met Ile Asn Gly Cys Tyr Asn Phe Thr Leu Asp Asp Ile Pro Val Val				
180 185 190				
ccg tat gta tgc gca gga ata gga gga gat ttc ata gag ttt ttt aat	624			
Pro Tyr Val Cys Ala Gly Ile Gly Gly Asp Phe Ile Glu Phe Phe Asn				

195

200

205

gat tta cat gtt aag ttt cgt cat caa ggc aag gta ggt att agt tat 672
 Asp Leu His Val Lys Phe Arg His Gln Gly Lys Val Gly Ile Ser Tyr
 210 215 220

tct ata tcc cct gaa gta agt tta ttt ctt aac gga tat tac cat aaa 720
 Ser Ile Ser Pro Glu Val Ser Leu Phe Leu Asn Gly Tyr Tyr His Lys
 225 230 235 240

gta aca ggt aac aga ttt aaa aac tta cac gtt caa cac gta agt gat 768
 Val Thr Gly Asn Arg Phe Lys Asn Leu His Val Gln His Val Ser Asp
 245 250 255

tta agt gac gct cct aag ttc aca tct gca gtt gct aca ctc aat gtt 816
 Leu Ser Asp Ala Pro Lys Phe Thr Ser Ala Val Ala Thr Leu Asn Val
 260 265 270

ggg tac ttt ggt ggc gaa att gga gta aga ttt ata ttt taa 858
 Gly Tyr Phe Gly Gly Glu Ile Gly Val Arg Phe Ile Phe
 275 280 285

<210> 30

<211> 285

<212> PRT

<213> Ehrlichia chaffeensis

<400> 30

Met Asn Asn Arg Lys Ser Phe Phe Ile Ile Gly Ala Ser Leu Leu Ala
 1 5 10 15

Ser Leu Leu Phe Thr Ser Glu Ala Ser Ser Thr Gly Asn Val Ser Asn
 20 25 30

His Thr Tyr Phe Lys Pro Arg Leu Tyr Ile Ser Gly Gln Tyr Arg Pro
 35 40 45

Gly Val Ser His Phe Ser Lys Phe Ser Val Lys Glu Thr Asn Tyr Asn
 50 55 60

Thr Thr Gln Leu Val Gly Leu Lys Lys Asp Ile Ser Val Ile Gly Asn
 65 70 75 80

Ser Asn Ile Thr Thr Tyr Thr Asn Phe Asn Phe Pro Tyr Ile Ala Glu
 85 90 95

Phe Gln Asp Asn Ala Ile Ser Phe Ser Gly Ala Ile Gly Tyr Leu Tyr

100	105	110
Ser Glu Asn Phe Arg Ile Glu Val Glu Ala Ser Tyr Glu Glu Phe Asp		
115	120	125
Val Lys Asn Pro Glu Gly Ser Ala Thr Asp Ala Tyr Arg Tyr Phe Ala		
130	135	140
Leu Ala Arg Ala Met Asp Gly Thr Asn Lys Ser Ser Pro Asp Asp Thr		
145	150	155
Arg Lys Phe Thr Val Met Arg Asn Asp Gly Leu Ser Ile Ser Ser Val		
165	170	175
Met Ile Asn Gly Cys Tyr Asn Phe Thr Leu Asp Asp Ile Pro Val Val		
180	185	190
Pro Tyr Val Cys Ala Gly Ile Gly Gly Asp Phe Ile Glu Phe Phe Asn		
195	200	205
Asp Leu His Val Lys Phe Arg His Gln Gly Lys Val Gly Ile Ser Tyr		
210	215	220
Ser Ile Ser Pro Glu Val Ser Leu Phe Leu Asn Gly Tyr Tyr His Lys		
225	230	235
Val Thr Gly Asn Arg Phe Lys Asn Leu His Val Gln His Val Ser Asp		
245	250	255
Leu Ser Asp Ala Pro Lys Phe Thr Ser Ala Val Ala Thr Leu Asn Val		
260	265	270
Gly Tyr Phe Gly Gly Glu Ile Gly Val Arg Phe Ile Phe		
275	280	285

<210> 31

<211> 867

<212> DNA

<213> Ehrlichia canis.

<220>

<221> CDS

<222> (1)..(867)

<400> 31

atg aat tgc aaa aga ttt ttc ata gca agt gca ttg ata tca cta atg 48
Met Asn Cys Lys Arg Phe Phe Ile Ala Ser Ala Leu Ile Ser Leu Met

1	5	10	15	
tct ttc tta cct agc gta tct ttt tct gaa tca ata cat gaa gat aat	96			
Ser Phe Leu Pro Ser Val Ser Phe Ser Glu Ser Ile His Glu Asp Asn				
20	25	30		
ata aat ggt aac ttt tac att agt gca aag tat atg cca agt gcc tca	144			
Ile Asn Gly Asn Phe Tyr Ile Ser Ala Lys Tyr Met Pro Ser Ala Ser				
35	40	45		
cac ttt ggc gta ttt tca gtt aaa gaa gag aaa aac aca aca act gga	192			
His Phe Gly Val Phe Ser Val Lys Glu Glu Lys Asn Thr Thr Thr Gly				
50	55	60		
gtt ttc gga tta aaa caa gat tgg gac gga gca aca ata aag gat gca	240			
Val Phe Gly Leu Lys Gln Asp Trp Asp Gly Ala Thr Ile Lys Asp Ala				
65	70	75	80	
agc agc agc cac aca ata gac cca agt aca ata ttc tcc att tca aat	288			
Ser Ser Ser His Thr Ile Asp Pro Ser Thr Ile Phe Ser Ile Ser Asn				
85	90	95		
tat tca ttt aaa tat gaa aac aat cca ttt tta ggg ttt gca gga gct	336			
Tyr Ser Phe Lys Tyr Glu Asn Asn Pro Phe Leu Gly Phe Ala Gly Ala				
100	105	110		
att ggc tac tca atg ggt ggt cca agg gta gag ttt gaa gtg tct tac	384			
Ile Gly Tyr Ser Met Gly Gly Pro Arg Val Glu Phe Glu Val Ser Tyr				
115	120	125		
gaa ata ttt gat gta aaa aac caa ggt aac agt tac aag aac gat gct	432			
Glu Ile Phe Asp Val Lys Asn Gln Gly Asn Ser Tyr Lys Asn Asp Ala				
130	135	140		
cac aaa tat tgc gct tta tca aga cac acc gga ggt atg cca caa gcc	480			
His Lys Tyr Cys Ala Leu Ser Arg His Thr Gly Gly Met Pro Gln Ala				
145	150	155	160	
ggt cat caa aat aaa ttt gtc ttc cta aaa aat gaa gga tta ctt gac	528			
Gly His Gln Asn Lys Phe Val Phe Leu Lys Asn Glu Gly Leu Leu Asp				
165	170	175		
ata tca ctt atg ata aac gca tgt tat gat ata aca atc gac agc atg	576			
Ile Ser Leu Met Ile Asn Ala Cys Tyr Asp Ile Thr Ile Asp Ser Met				
180	185	190		
cca ttt tct cca tat ata tgt gca ggt att ggt agt gac tta gtt tcg	624			
Pro Phe Ser Pro Tyr Ile Cys Ala Gly Ile Gly Ser Asp Leu Val Ser				

195 200 205
 atg ttt gaa act aca aat cct aaa att tct tat caa gga aaa tta ggt 672
 Met Phe Glu Thr Thr Asn Pro Lys Ile Ser Tyr Gln Gly Lys Leu Gly
 210 215 220
 gta agt tac tcc ata agc cca gaa gca tct gtt ttt gtt gga gga cac 720
 Val Ser Tyr Ser Ile Ser Pro Glu Ala Ser Val Phe Val Gly Gly His
 225 230 235 240
 ttt cac aga gtt ata ggt aat gaa ttt aaa gac att cct gca ata act 768
 Phe His Arg Val Ile Gly Asn Glu Phe Lys Asp Ile Pro Ala Ile Thr
 245 250 255
 cct gct gga gca aca gaa att aaa ggc aca cag ttt aca aca gta aca 816
 Pro Ala Gly Ala Thr Glu Ile Lys Gly Thr Gln Phe Thr Thr Val Thr
 260 265 270
 tta aac ata tgc cac ttc gga cta gag ctt gga ggc agg ttt act ttt 864
 Leu Asn Ile Cys His Phe Gly Leu Glu Leu Gly Gly Arg Phe Thr Phe
 275 280 285
 taa 867

<210> 32
 <211> 288
 <212> PRT
 <213> Ehrlichia canis

<400> 32
 Met Asn Cys Lys Arg Phe Phe Ile Ala Ser Ala Leu Ile Ser Leu Met
 1 5 10 15
 Ser Phe Leu Pro Ser Val Ser Phe Ser Glu Ser Ile His Glu Asp Asn
 20 25 30
 Ile Asn Gly Asn Phe Tyr Ile Ser Ala Lys Tyr Met Pro Ser Ala Ser
 35 40 45
 His Phe Gly Val Phe Ser Val Lys Glu Glu Lys Asn Thr Thr Thr Gly
 50 55 60
 Val Phe Gly Leu Lys Gln Asp Trp Asp Gly Ala Thr Ile Lys Asp Ala
 65 70 75 80
 Ser Ser Ser His Thr Ile Asp Pro Ser Thr Ile Phe Ser Ile Ser Asn

	85		90		95
Tyr Ser Phe Lys Tyr Glu Asn Asn Pro Phe Leu Gly Phe Ala Gly Ala	100		105		110
Ile Gly Tyr Ser Met Gly Gly Pro Arg Val Glu Phe Glu Val Ser Tyr	115		120		125
Glu Ile Phe Asp Val Lys Asn Gln Gly Asn Ser Tyr Lys Asn Asp Ala	130		135		140
His Lys Tyr Cys Ala Leu Ser Arg His Thr Gly Gly Met Pro Gln Ala	145		150		155
					160
Gly His Gln Asn Lys Phe Val Phe Leu Lys Asn Glu Gly Leu Leu Asp		165		170	175
Ile Ser Leu Met Ile Asn Ala Cys Tyr Asp Ile Thr Ile Asp Ser Met	180		185		190
Pro Phe Ser Pro Tyr Ile Cys Ala Gly Ile Gly Ser Asp Leu Val Ser	195		200		205
Met Phe Glu Thr Thr Asn Pro Lys Ile Ser Tyr Gln Gly Lys Leu Gly	210		215		220
Val Ser Tyr Ser Ile Ser Pro Glu Ala Ser Val Phe Val Gly Gly His	225		230		235
					240
Phe His Arg Val Ile Gly Asn Glu Phe Lys Asp Ile Pro Ala Ile Thr	245		250		255
Pro Ala Gly Ala Thr Glu Ile Lys Gly Thr Gln Phe Thr Thr Val Thr	260		265		270
Leu Asn Ile Cys His Phe Gly Leu Glu Leu Gly Gly Arg Phe Thr Phe	275		280		285

<210> 33

<211> 864

<212> DNA

<213> Ehrlichia chaffeensis

<220>

<221> CDS

<222> (1)..(864)

<400> 33

atg aaa tat aaa aaa act ttt aca gta act gca tta gta tta tta act	48
Met Lys Tyr Lys Lys Thr Phe Thr Val Thr Ala Leu Val Leu Leu Thr	
1 5 10 15	
tcc ttt aca cat ttt ata cct ttt tat agt cca gca cgt gcc agt aca	96
Ser Phe Thr His Phe Ile Pro Phe Tyr Ser Pro Ala Arg Ala Ser Thr	
20 25 30	
att cac aac ttc tac att agt gga aaa tat atg cca aca gcg tca cat	144
Ile His Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro Thr Ala Ser His	
35 40 45	
ttt gga att ttt tca gct aaa gaa gaa caa agt ttt act aag gta tta	192
Phe Gly Ile Phe Ser Ala Lys Glu Glu Gln Ser Phe Thr Lys Val Leu	
50 55 60	
gtt ggg tta gat caa cga tta tca cat aat att ata aac aat aat gat	240
Val Gly Leu Asp Gln Arg Leu Ser His Asn Ile Ile Asn Asn Asn Asp	
65 70 75 80	
aca gca aag agt ctt aag gtt caa aat tat tca ttt aaa tac aaa aat	288
Thr Ala Lys Ser Leu Lys Val Gln Asn Tyr Ser Phe Lys Tyr Lys Asn	
85 90 95	
aac cca ttt cta gga ttt gca aga gct att ggt tat tca ata ggc aat	336
Asn Pro Phe Leu Gly Phe Ala Arg Ala Ile Gly Tyr Ser Ile Gly Asn	
100 105 110	
tca aga ata gaa cta gaa gta tca cat gaa ata ttt gat act aaa aac	384
Ser Arg Ile Glu Leu Glu Val Ser His Glu Ile Phe Asp Thr Lys Asn	
115 120 125	
cca gga aac aat tat tta aat gac tct cac aaa tat tgc gct tta tct	432
Pro Gly Asn Asn Tyr Leu Asn Asp Ser His Lys Tyr Cys Ala Leu Ser	
130 135 140	
cat gga agt cac ata tgc agt gat gga aat agc gga gat tgg tac act	480
His Gly Ser His Ile Cys Ser Asp Gly Asn Ser Gly Asp Trp Tyr Thr	
145 150 155 160	
gca aaa act gat aag ttt gta ctt ctg aaa aat gaa ggt tta ctt gac	528
Ala Lys Thr Asp Lys Phe Val Leu Leu Lys Asn Glu Gly Leu Leu Asp	
165 170 175	
gtc tca ttt atg tta aac gca tgt tat gac ata aca act gaa aaa atg	576
Val Ser Phe Met Leu Asn Ala Cys Tyr Asp Ile Thr Thr Glu Lys Met	
180 185 190	

cct ttt tca cct tat ata tgt gca ggt att ggt act gat ctc ata tct 624
 Pro Phe Ser Pro Tyr Ile Cys Ala Gly Ile Gly Thr Asp Leu Ile Ser
 195 200 205

atg ttt gag aca aca caa aac aaa ata tct tat caa gga aag tta ggt 672
 Met Phe Glu Thr Thr Gln Asn Lys Ile Ser Tyr Gln Gly Lys Leu Gly
 210 215 220

tta aac tat act ata aac tca aga gtt tct gtt ttt gca ggt ggg cac 720
 Leu Asn Tyr Thr Ile Asn Ser Arg Val Ser Val Phe Ala Gly Gly His
 225 230 235 240

ttt cat aaa gta ata ggt aat gaa ttt aaa ggt att cct act cta tta 768
 Phe His Lys Val Ile Gly Asn Glu Phe Lys Gly Ile Pro Thr Leu Leu
 245 250 255

cct gat gga tca aac att aaa gta caa cag tct gca aca gta aca tta 816
 Pro Asp Gly Ser Asn Ile Lys Val Gln Gln Ser Ala Thr Val Thr Leu
 260 265 270

gat gtg tgc cat ttc ggg tta gag att gga agt aga ttt ttc ttt taa 864
 Asp Val Cys His Phe Gly Leu Glu Ile Gly Ser Arg Phe Phe Phe
 275 280 285

<210> 34

<211> 287

<212> PRT

<213> Ehrlichia chaffeensis

<400> 34

Met Lys Tyr Lys Lys Thr Phe Thr Val Thr Ala Leu Val Leu Leu Thr
 1 5 10 15

Ser Phe Thr His Phe Ile Pro Phe Tyr Ser Pro Ala Arg Ala Ser Thr
 20 25 30

Ile His Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro Thr Ala Ser His
 35 40 45

Phe Gly Ile Phe Ser Ala Lys Glu Glu Gln Ser Phe Thr Lys Val Leu
 50 55 60

Val Gly Leu Asp Gln Arg Leu Ser His Asn Ile Ile Asn Asn Asn Asp
 65 70 75 80

Thr Ala Lys Ser Leu Lys Val Gln Asn Tyr Ser Phe Lys Tyr Lys Asn

85	90	95
Asn Pro Phe Leu Gly Phe Ala Arg Ala Ile Gly Tyr Ser Ile Gly Asn		
100	105	110
Ser Arg Ile Glu Leu Glu Val Ser His Glu Ile Phe Asp Thr Lys Asn		
115	120	125
Pro Gly Asn Asn Tyr Leu Asn Asp Ser His Lys Tyr Cys Ala Leu Ser		
130	135	140
His Gly Ser His Ile Cys Ser Asp Gly Asn Ser Gly Asp Trp Tyr Thr		
145	150	155
Ala Lys Thr Asp Lys Phe Val Leu Leu Lys Asn Glu Gly Leu Leu Asp		
165	170	175
Val Ser Phe Met Leu Asn Ala Cys Tyr Asp Ile Thr Thr Glu Lys Met		
180	185	190
Pro Phe Ser Pro Tyr Ile Cys Ala Gly Ile Gly Thr Asp Leu Ile Ser		
195	200	205
Met Phe Glu Thr Thr Gln Asn Lys Ile Ser Tyr Gln Gly Lys Leu Gly		
210	215	220
Leu Asn Tyr Thr Ile Asn Ser Arg Val Ser Val Phe Ala Gly Gly His		
225	230	235
Phe His Lys Val Ile Gly Asn Glu Phe Lys Gly Ile Pro Thr Leu Leu		
245	250	255
Pro Asp Gly Ser Asn Ile Lys Val Gln Gln Ser Ala Thr Val Thr Leu		
260	265	270
Asp Val Cys His Phe Gly Leu Glu Ile Gly Ser Arg Phe Phe Phe		
275	280	285

<210> 35

<211> 924

<212> DNA

<213> Ehrlichia canis

<220>

<221> CDS

<222> (1)..(924)

<400> 35

atg ttt tat act aat ata tat att ctg gct tgt att tac ttt gca ctt	48
Met Phe Tyr Thr Asn Ile Tyr Ile Leu Ala Cys Ile Tyr Phe Ala Leu	
1 5 10 15	
cca cta ttg tta att tat ttt cac tat ttt agg tgt aat atg aat tgc	96
Pro Leu Leu Leu Ile Tyr Phe His Tyr Phe Arg Cys Asn Met Asn Cys	
20 25 30	
aaa aaa att ctt ata aca act gca tta ata tca tta atg tac tct att	144
Lys Lys Ile Leu Ile Thr Thr Ala Leu Ile Ser Leu Met Tyr Ser Ile	
35 40 45	
cca agc ata tct ttt tct gat act ata caa gat ggt aac atg ggt ggt	192
Pro Ser Ile Ser Phe Ser Asp Thr Ile Gln Asp Gly Asn Met Gly Gly	
50 55 60	
aac ttc tat att agt gga aag tat gta cca agt gtc tca cat ttt ggt	240
Asn Phe Tyr Ile Ser Gly Lys Tyr Val Pro Ser Val Ser His Phe Gly	
65 70 75 80	
agc ttc tca gct aaa gaa gaa agc aaa tca act gtt gga gtt ttt gga	288
Ser Phe Ser Ala Lys Glu Glu Ser Lys Ser Thr Val Gly Val Phe Gly	
85 90 95	
tta aaa cat gat tgg gat gga agt cca ata ctt aag aat aaa cac gct	336
Leu Lys His Asp Trp Asp Gly Ser Pro Ile Leu Lys Asn Lys His Ala	
100 105 110	
gac ttt act gtt cca aac tat tct ttc aga tac gag aac aat cca ttt	384
Asp Phe Thr Val Pro Asn Tyr Ser Phe Arg Tyr Glu Asn Asn Pro Phe	
115 120 125	
cta ggg ttt gca gga gct atc ggt tac tca atg ggt ggc cca aga ata	432
Leu Gly Phe Ala Gly Ala Ile Gly Tyr Ser Met Gly Gly Pro Arg Ile	
130 135 140	
gaa ttc gaa ata tct tat gaa gca ttc gac gta aaa agt cct aat atc	480
Glu Phe Glu Ile Ser Tyr Glu Ala Phe Asp Val Lys Ser Pro Asn Ile	
145 150 155 160	
aat tat caa aat gac gcg cac agg tac tgc gct cta tct cat cac aca	528
Asn Tyr Gln Asn Asp Ala His Arg Tyr Cys Ala Leu Ser His His Thr	
165 170 175	
tcg gca gcc atg gaa gct gat aaa ttt gtc ttc tta aaa aac gaa ggg	576
Ser Ala Ala Met Glu Ala Asp Lys Phe Val Phe Leu Lys Asn Glu Gly	
180 185 190	

tta att gac ata tca ctt gca ata aat gca tgt tat gat ata ata aat 624
 Leu Ile Asp Ile Ser Leu Ala Ile Asn Ala Cys Tyr Asp Ile Ile Asn
 195 200 205

gac aaa gta cct gtt tct cct tat ata tgc gca ggt att ggt act gat 672
 Asp Lys Val Pro Val Ser Pro Tyr Ile Cys Ala Gly Ile Gly Thr Asp
 210 215 220

ttg att tct atg ttt gaa gct aca agt cct aaa att tcc tac caa gga 720
 Leu Ile Ser Met Phe Glu Ala Thr Ser Pro Lys Ile Ser Tyr Gln Gly
 225 230 235 240

aaa ctg ggc att agt tac tct att aat ccg gaa acc tct gtt ttc atc 768
 Lys Leu Gly Ile Ser Tyr Ser Ile Asn Pro Glu Thr Ser Val Phe Ile
 245 250 255

ggt ggg cat ttc cac agg atc ata ggt aat gag ttt aga gat att cct 816
 Gly Gly His Phe His Arg Ile Ile Gly Asn Glu Phe Arg Asp Ile Pro
 260 265 270

gca ata gta cct agt aac tca act aca ata agt gga cca caa ttt gca 864
 Ala Ile Val Pro Ser Asn Ser Thr Thr Ile Ser Gly Pro Gln Phe Ala
 275 280 285

aca gta aca cta aat gtg tgt cac ttt ggt tta gaa ctt gga gga aga 912
 Thr Val Thr Leu Asn Val Cys His Phe Gly Leu Glu Leu Gly Gly Arg
 290 295 300

ttt aac ttc taa 924
 Phe Asn Phe
 305

<210> 36
 <211> 307
 <212> PRT
 <213> Ehrlichia canis

<400> 36
 Met Phe Tyr Thr Asn Ile Tyr Ile Leu Ala Cys Ile Tyr Phe Ala Leu
 1 5 10 15

Pro Leu Leu Leu Ile Tyr Phe His Tyr Phe Arg Cys Asn Met Asn Cys
 20 25 30

Lys Lys Ile Leu Ile Thr Thr Ala Leu Ile Ser Leu Met Tyr Ser Ile
 35 40 45

Pro Ser Ile Ser Phe Ser Asp Thr Ile Gln Asp Gly Asn Met Gly Gly
 50 55 60

Asn Phe Tyr Ile Ser Gly Lys Tyr Val Pro Ser Val Ser His Phe Gly
 65 70 75 80

Ser Phe Ser Ala Lys Glu Glu Ser Lys Ser Thr Val Gly Val Phe Gly
 85 90 95

Leu Lys His Asp Trp Asp Gly Ser Pro Ile Leu Lys Asn Lys His Ala
 100 105 110

Asp Phe Thr Val Pro Asn Tyr Ser Phe Arg Tyr Glu Asn Asn Pro Phe
 115 120 125

Leu Gly Phe Ala Gly Ala Ile Gly Tyr Ser Met Gly Gly Pro Arg Ile
 130 135 140

Glu Phe Glu Ile Ser Tyr Glu Ala Phe Asp Val Lys Ser Pro Asn Ile
 145 150 155 160

Asn Tyr Gln Asn Asp Ala His Arg Tyr Cys Ala Leu Ser His His Thr
 165 170 175

Ser Ala Ala Met Glu Ala Asp Lys Phe Val Phe Leu Lys Asn Glu Gly
 180 185 190

Leu Ile Asp Ile Ser Leu Ala Ile Asn Ala Cys Tyr Asp Ile Ile Asn
 195 200 205

Asp Lys Val Pro Val Ser Pro Tyr Ile Cys Ala Gly Ile Gly Thr Asp
 210 215 220

Leu Ile Ser Met Phe Glu Ala Thr Ser Pro Lys Ile Ser Tyr Gln Gly
 225 230 235 240

Lys Leu Gly Ile Ser Tyr Ser Ile Asn Pro Glu Thr Ser Val Phe Ile
 245 250 255

Gly Gly His Phe His Arg Ile Ile Gly Asn Glu Phe Arg Asp Ile Pro
 260 265 270

Ala Ile Val Pro Ser Asn Ser Thr Thr Ile Ser Gly Pro Gln Phe Ala
 275 280 285

Thr Val Thr Leu Asn Val Cys His Phe Gly Leu Glu Leu Gly Gly Arg
 290 295 300

Phe Asn Phe
305

<210> 37

<211> 843

<212> DNA

<213> Ehrlichia canis

<220>

<221> CDS

<222> (1)..(843)

<400> 37

atg aat tgc aaa aaa att ctt ata aca act gca tta atg tca tta atg 48
Met Asn Cys Lys Lys Ile Leu Ile Thr Thr Ala Leu Met Ser Leu Met
1 5 10 15

tac tat gct cca agc ata tct ttt tct gat act ata caa gac gat aac 96
Tyr Tyr Ala Pro Ser Ile Ser Phe Ser Asp Thr Ile Gln Asp Asp Asn
20 25 30

act ggt agc ttc tac atc agt gga aaa tat gta cca agt gtt tca cat 144
Thr Gly Ser Phe Tyr Ile Ser Gly Lys Tyr Val Pro Ser Val Ser His
35 40 45

ttt ggt gtt ttc tca gct aaa gaa gaa aga aac tca act gtt gga gtt 192
Phe Gly Val Phe Ser Ala Lys Glu Glu Arg Asn Ser Thr Val Gly Val
50 55 60

ttt gga tta aaa cat gat tgg aat gga ggt aca ata tct aac tct tct 240
Phe Gly Leu Lys His Asp Trp Asn Gly Gly Thr Ile Ser Asn Ser Ser
65 70 75 80

cca gaa aat ata ttc aca gtt caa aat tat tcg ttt aaa tac gaa aac 288
Pro Glu Asn Ile Phe Thr Val Gln Asn Tyr Ser Phe Lys Tyr Glu Asn
85 90 95

aac cca ttc tta ggg ttt gca gga gct att ggt tat tca atg ggt ggc 336
Asn Pro Phe Leu Gly Phe Ala Gly Ala Ile Gly Tyr Ser Met Gly Gly
100 105 110

cca aga ata gaa ctt gaa gtt ctg tac gag aca ttc gat gtg aaa aat 384
Pro Arg Ile Glu Leu Glu Val Leu Tyr Glu Thr Phe Asp Val Lys Asn
115 120 125

cag aac aat aat tat aag aac ggc gca cac aga tac tgt gct tta tct 432

Tyr Tyr Ala Pro Ser Ile Ser Phe Ser Asp Thr Ile Gln Asp Asp Asn
 20 25 30

Thr Gly Ser Phe Tyr Ile Ser Gly Lys Tyr Val Pro Ser Val Ser His
 35 40 45

Phe Gly Val Phe Ser Ala Lys Glu Glu Arg Asn Ser Thr Val Gly Val
 50 55 60

Phe Gly Leu Lys His Asp Trp Asn Gly Gly Thr Ile Ser Asn Ser Ser
 65 70 75 80

Pro Glu Asn Ile Phe Thr Val Gln Asn Tyr Ser Phe Lys Tyr Glu Asn
 85 90 95

Asn Pro Phe Leu Gly Phe Ala Gly Ala Ile Gly Tyr Ser Met Gly Gly
 100 105 110

Pro Arg Ile Glu Leu Glu Val Leu Tyr Glu Thr Phe Asp Val Lys Asn
 115 120 125

Gln Asn Asn Asn Tyr Lys Asn Gly Ala His Arg Tyr Cys Ala Leu Ser
 130 135 140

His His Ser Ser Ala Thr Asn Met Ser Ser Ala Ser Asn Lys Phe Val
 145 150 155 160

Phe Leu Lys Asn Glu Gly Leu Ile Asp Leu Ser Phe Met Ile Asn Ala
 165 170 175

Cys Tyr Asp Ile Ile Ile Glu Gly Met Pro Phe Ser Pro Tyr Ile Cys
 180 185 190

Ala Gly Val Gly Thr Asp Val Val Ser Met Phe Glu Ala Ile Asn Pro
 195 200 205

Lys Ile Ser Tyr Gln Gly Lys Leu Gly Leu Gly Tyr Ser Ile Ser Ser
 210 215 220

Glu Ala Ser Val Phe Ile Gly Gly His Phe His Arg Val Ile Gly Asn
 225 230 235 240

Glu Phe Arg Asp Ile Pro Ala Met Val Pro Ser Gly Ser Asn Leu Pro
 245 250 255

Glu Asn Gln Phe Ala Ile Val Thr Leu Asn Val Cys His Phe Gly Leu
 260 265 270

Glu Leu Gly Gly Arg Phe Asn Phe
 275 280

<210> 39
 <211> 852
 <212> DNA
 <213> Ehrlichia canis

<220>
 <221> CDS
 <222> (1)..(852)

<400> 39
 atg aat tgt aaa aaa gtt ttc aca ata agt gca ttg ata tca tcc ata 48
 Met Asn Cys Lys Lys Val Phe Thr Ile Ser Ala Leu Ile Ser Ser Ile
 1 5 10 15
 tac ttc cta cct aat gtc tca tac tct aac cca gta tat ggt aac agt 96
 Tyr Phe Leu Pro Asn Val Ser Tyr Ser Asn Pro Val Tyr Gly Asn Ser
 20 25 30
 atg tat ggt aat ttt tac ata tca gga aag tac atg cca agt gtt cct 144
 Met Tyr Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro Ser Val Pro
 35 40 45
 cat ttt gga att ttt tca gct gaa gaa gag aaa aaa aag aca act gta 192
 His Phe Gly Ile Phe Ser Ala Glu Glu Glu Lys Lys Lys Thr Thr Val
 50 55 60
 gta tat ggc tta aaa gga aaa ctg gca gga gat gca ata tct agt caa 240
 Val Tyr Gly Leu Lys Gly Lys Leu Ala Gly Asp Ala Ile Ser Ser Gln
 65 70 75 80
 agt cca gat gat aat ttt acc att cga aat tac tca ttc aag tat gca 288
 Ser Pro Asp Asp Asn Phe Thr Ile Arg Asn Tyr Ser Phe Lys Tyr Ala
 85 90 95
 agc aac aag ttt tta ggg ttt gca gta gct att ggt tac tcg ata ggc 336
 Ser Asn Lys Phe Leu Gly Phe Ala Val Ala Ile Gly Tyr Ser Ile Gly
 100 105 110
 agt cca aga ata gaa gtt gag atg tct tat gaa gca ttt gat gtg aaa 384
 Ser Pro Arg Ile Glu Val Glu Met Ser Tyr Glu Ala Phe Asp Val Lys
 115 120 125
 aat cca ggt gat aat tac aaa aac ggt gct tac agg tat tgt gct tta 432

Asn Pro Gly Asp Asn Tyr Lys Asn Gly Ala Tyr Arg Tyr Cys Ala Leu
 130 135 140

tct cat caa gat gat gcg gat gat gac atg act agt gca act gac aaa 480
 Ser His Gln Asp Asp Ala Asp Asp Asp Met Thr Ser Ala Thr Asp Lys
 145 150 155 160

ttt gta tat tta att aat gaa gga tta ctt aac ata tca ttt atg aca 528
 Phe Val Tyr Leu Ile Asn Glu Gly Leu Leu Asn Ile Ser Phe Met Thr
 165 170 175

aac ata tgt tat gaa aca gca agc aaa aat ata cct ctc tct cct tac 576
 Asn Ile Cys Tyr Glu Thr Ala Ser Lys Asn Ile Pro Leu Ser Pro Tyr
 180 185 190

ata tgt gca ggt att ggt act gat tta att cac atg ttt gaa act aca 624
 Ile Cys Ala Gly Ile Gly Thr Asp Leu Ile His Met Phe Glu Thr Thr
 195 200 205

cat cct aaa att tct tat caa gga aag cta ggg ttg gcc tac ttc gta 672
 His Pro Lys Ile Ser Tyr Gln Gly Lys Leu Gly Leu Ala Tyr Phe Val
 210 215 220

agt gca gag tct tcg gtt tct ttt ggt ata tat ttt cat aaa att ata 720
 Ser Ala Glu Ser Ser Val Ser Phe Gly Ile Tyr Phe His Lys Ile Ile
 225 230 235 240

aat aat aag ttt aaa aat gtt cca gcc atg gta cct att aac tca gac 768
 Asn Asn Lys Phe Lys Asn Val Pro Ala Met Val Pro Ile Asn Ser Asp
 245 250 255

gag ata gta gga cca cag ttt gca aca gta aca tta aat gta tgc tac 816
 Glu Ile Val Gly Pro Gln Phe Ala Thr Val Thr Leu Asn Val Cys Tyr
 260 265 270

ttt gga tta gaa ctt gga tgt agg ttc aac ttc taa 852
 Phe Gly Leu Glu Leu Gly Cys Arg Phe Asn Phe
 275 280

<210> 40

<211> 283

<212> PRT

<213> Ehrlichia canis

<400> 40

Met Asn Cys Lys Lys Val Phe Thr Ile Ser Ala Leu Ile Ser Ser Ile
 1 5 10 15

Tyr Phe Leu Pro Asn Val Ser Tyr Ser Asn Pro Val Tyr Gly Asn Ser
20 25 30

Met Tyr Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro Ser Val Pro
35 40 45

His Phe Gly Ile Phe Ser Ala Glu Glu Glu Lys Lys Lys Thr Thr Val
50 55 60

Val Tyr Gly Leu Lys Gly Lys Leu Ala Gly Asp Ala Ile Ser Ser Gln
65 70 75 80

Ser Pro Asp Asp Asn Phe Thr Ile Arg Asn Tyr Ser Phe Lys Tyr Ala
85 90 95

Ser Asn Lys Phe Leu Gly Phe Ala Val Ala Ile Gly Tyr Ser Ile Gly
100 105 110

Ser Pro Arg Ile Glu Val Glu Met Ser Tyr Glu Ala Phe Asp Val Lys
115 120 125

Asn Pro Gly Asp Asn Tyr Lys Asn Gly Ala Tyr Arg Tyr Cys Ala Leu
130 135 140

Ser His Gln Asp Asp Ala Asp Asp Asp Met Thr Ser Ala Thr Asp Lys
145 150 155 160

Phe Val Tyr Leu Ile Asn Glu Gly Leu Leu Asn Ile Ser Phe Met Thr
165 170 175

Asn Ile Cys Tyr Glu Thr Ala Ser Lys Asn Ile Pro Leu Ser Pro Tyr
180 185 190

Ile Cys Ala Gly Ile Gly Thr Asp Leu Ile His Met Phe Glu Thr Thr
195 200 205

His Pro Lys Ile Ser Tyr Gln Gly Lys Leu Gly Leu Ala Tyr Phe Val
210 215 220

Ser Ala Glu Ser Ser Val Ser Phe Gly Ile Tyr Phe His Lys Ile Ile
225 230 235 240

Asn Asn Lys Phe Lys Asn Val Pro Ala Met Val Pro Ile Asn Ser Asp
245 250 255

Glu Ile Val Gly Pro Gln Phe Ala Thr Val Thr Leu Asn Val Cys Tyr
260 265 270

Phe Gly Leu Glu Leu Gly Cys Arg Phe Asn Phe
 275 280

<210> 41
 <211> 831
 <212> DNA
 <213> Ehrlichia canis

<220>
 <221> CDS
 <222> (1)..(831)

<400> 41
 atg aac tgt aaa aaa ttt ctt ata aca act aca ttg gta tca cta aca 48
 Met Asn Cys Lys Lys Phe Leu Ile Thr Thr Thr Leu Val Ser Leu Thr
 1 5 10 15
 att ctt tta cct ggc ata tct ttc tcc aaa cca ata cat gaa aac aat 96
 Ile Leu Leu Pro Gly Ile Ser Phe Ser Lys Pro Ile His Glu Asn Asn
 20 25 30
 act aca gga aac ttt tac att att gga aaa tat gta cca agt att tca 144
 Thr Thr Gly Asn Phe Tyr Ile Ile Gly Lys Tyr Val Pro Ser Ile Ser
 35 40 45
 cat ttt ggg aac ttt tca gct aaa gaa gaa aaa aac aca act act gga 192
 His Phe Gly Asn Phe Ser Ala Lys Glu Glu Lys Asn Thr Thr Thr Gly
 50 55 60
 att ttt gga tta aaa gaa tca tgg act ggt ggt atc atc ctt gat aaa 240
 Ile Phe Gly Leu Lys Glu Ser Trp Thr Gly Gly Ile Ile Leu Asp Lys
 65 70 75 80
 gaa cat gca gct ttt aat atc cca aat tat tca ttt aaa tat gaa aat 288
 Glu His Ala Ala Phe Asn Ile Pro Asn Tyr Ser Phe Lys Tyr Glu Asn
 85 90 95
 aat cca ttt tta gga ttt gca ggg gta att ggc tat tca ata ggt agt 336
 Asn Pro Phe Leu Gly Phe Ala Gly Val Ile Gly Tyr Ser Ile Gly Ser
 100 105 110
 cca aga ata gaa ttt gaa gta tca tac gag aca ttc gat gta caa aat 384
 Pro Arg Ile Glu Phe Glu Val Ser Tyr Glu Thr Phe Asp Val Gln Asn
 115 120 125
 cca gga gat aag ttt aac aat gat gca cat aag tat tgt gct tta tcc 432

Pro Gly Asp Lys Phe Asn Asn Asp Ala His Lys Tyr Cys Ala Leu Ser
 130 135 140

aat gat tcc agt aaa aca atg aaa agt ggt aaa ttc gtt ttt ctc aaa 480
 Asn Asp Ser Ser Lys Thr Met Lys Ser Gly Lys Phe Val Phe Leu Lys
 145 150 155 160

aat gaa gga tta agt gac ata tca ctc atg tta aat gta tgt tat gat 528
 Asn Glu Gly Leu Ser Asp Ile Ser Leu Met Leu Asn Val Cys Tyr Asp
 165 170 175

ata ata aac aaa aga atg cct ttt tca cct tac ata tgt gca ggc att 576
 Ile Ile Asn Lys Arg Met Pro Phe Ser Pro Tyr Ile Cys Ala Gly Ile
 180 185 190

ggt act gac tta ata ttc atg ttt gac gct ata aac cat aaa gct gct 624
 Gly Thr Asp Leu Ile Phe Met Phe Asp Ala Ile Asn His Lys Ala Ala
 195 200 205

tat caa gga aaa tta ggt ttt aat tat cca ata agc cca gaa gct aac 672
 Tyr Gln Gly Lys Leu Gly Phe Asn Tyr Pro Ile Ser Pro Glu Ala Asn
 210 215 220

att tct atg ggt gtg cac ttt cac aaa gta aca aac aac gag ttt aga 720
 Ile Ser Met Gly Val His Phe His Lys Val Thr Asn Asn Glu Phe Arg
 225 230 235 240

gtt cct gtt cta tta act gct gga gga ctc gct cca gat aat cta ttt 768
 Val Pro Val Leu Leu Thr Ala Gly Gly Leu Ala Pro Asp Asn Leu Phe
 245 250 255

gca ata gta aag ttg agt ata tgt cat ttt ggg tta gaa ttt ggg tac 816
 Ala Ile Val Lys Leu Ser Ile Cys His Phe Gly Leu Glu Phe Gly Tyr
 260 265 270

agg gtc agt ttt taa 831
 Arg Val Ser Phe
 275

<210> 42

<211> 276

<212> PRT

<213> Ehrlichia canis

<400> 42

Met Asn Cys Lys Lys Phe Leu Ile Thr Thr Thr Leu Val Ser Leu Thr
 1 5 10 15

Ile Leu Leu Pro Gly Ile Ser Phe Ser Lys Pro Ile His Glu Asn Asn
 20 25 30

Thr Thr Gly Asn Phe Tyr Ile Ile Gly Lys Tyr Val Pro Ser Ile Ser
 35 40 45

His Phe Gly Asn Phe Ser Ala Lys Glu Glu Lys Asn Thr Thr Thr Gly
 50 55 60

Ile Phe Gly Leu Lys Glu Ser Trp Thr Gly Gly Ile Ile Leu Asp Lys
 65 70 75 80

Glu His Ala Ala Phe Asn Ile Pro Asn Tyr Ser Phe Lys Tyr Glu Asn
 85 90 95

Asn Pro Phe Leu Gly Phe Ala Gly Val Ile Gly Tyr Ser Ile Gly Ser
 100 105 110

Pro Arg Ile Glu Phe Glu Val Ser Tyr Glu Thr Phe Asp Val Gln Asn
 115 120 125

Pro Gly Asp Lys Phe Asn Asn Asp Ala His Lys Tyr Cys Ala Leu Ser
 130 135 140

Asn Asp Ser Ser Lys Thr Met Lys Ser Gly Lys Phe Val Phe Leu Lys
 145 150 155 160

Asn Glu Gly Leu Ser Asp Ile Ser Leu Met Leu Asn Val Cys Tyr Asp
 165 170 175

Ile Ile Asn Lys Arg Met Pro Phe Ser Pro Tyr Ile Cys Ala Gly Ile
 180 185 190

Gly Thr Asp Leu Ile Phe Met Phe Asp Ala Ile Asn His Lys Ala Ala
 195 200 205

Tyr Gln Gly Lys Leu Gly Phe Asn Tyr Pro Ile Ser Pro Glu Ala Asn
 210 215 220

Ile Ser Met Gly Val His Phe His Lys Val Thr Asn Asn Glu Phe Arg
 225 230 235 240

Val Pro Val Leu Leu Thr Ala Gly Gly Leu Ala Pro Asp Asn Leu Phe
 245 250 255

Ala Ile Val Lys Leu Ser Ile Cys His Phe Gly Leu Glu Phe Gly Tyr
 260 265 270

Arg Val Ser Phe
275

<210> 43
<211> 882
<212> DNA
<213> Ehrlichia canis

<220>
<221> CDS
<222> (1)..(882)

<400> 43
atg aat aat aaa ctc aaa ttt act ata ata aac aca gta tta gta tgc 48
Met Asn Asn Lys Leu Lys Phe Thr Ile Ile Asn Thr Val Leu Val Cys
1 5 10 15

tta ttg tca tta cct aat ata tct tcc tca aag gcc ata aac aat aac 96
Leu Leu Ser Leu Pro Asn Ile Ser Ser Ser Lys Ala Ile Asn Asn Asn
20 25 30

gct aaa aag tac tac gga tta tat atc agt gga caa tat aaa ccc agt 144
Ala Lys Lys Tyr Tyr Gly Leu Tyr Ile Ser Gly Gln Tyr Lys Pro Ser
35 40 45

gtt tct gtt ttc agt aat ttt tca gtt aaa gaa acc aat gtc ata act 192
Val Ser Val Phe Ser Asn Phe Ser Val Lys Glu Thr Asn Val Ile Thr
50 55 60

aaa aac ctt ata gct tta aaa aaa gat gtt gac tct att gaa acc aag 240
Lys Asn Leu Ile Ala Leu Lys Lys Asp Val Asp Ser Ile Glu Thr Lys
65 70 75 80

act gat gcc agt gta ggt att agt aac cca tca aat ttt act atc ccc 288
Thr Asp Ala Ser Val Gly Ile Ser Asn Pro Ser Asn Phe Thr Ile Pro
85 90 95

tat aca gct gta ttt caa gat aat tct gtc aat ttc aat gga act att 336
Tyr Thr Ala Val Phe Gln Asp Asn Ser Val Asn Phe Asn Gly Thr Ile
100 105 110

ggt tac acc ttt gct gaa ggt aca aga gtt gaa ata gaa ggt tct tat 384
Gly Tyr Thr Phe Ala Glu Gly Thr Arg Val Glu Ile Glu Gly Ser Tyr
115 120 125

gag gaa ttt gat gtt aaa aac cct gga ggc tat aca cta agt gat gcc 432

Glu Glu Phe Asp Val Lys Asn Pro Gly Gly Tyr Thr Leu Ser Asp Ala
 130 135 140

tat cgc tat ttt gca tta gca cgt gaa atg aaa ggt aat agt ttt aca 480
 Tyr Arg Tyr Phe Ala Leu Ala Arg Glu Met Lys Gly Asn Ser Phe Thr
 145 150 155 160

cct aaa gaa aaa gtt tct aat agt ttt ttt cac act gta atg aga aat 528
 Pro Lys Glu Lys Val Ser Asn Ser Phe Phe His Thr Val Met Arg Asn
 165 170 175

gat gga tta tct ata ata tct gtt ata gta aat gtt tgc tac gat ttc 576
 Asp Gly Leu Ser Ile Ile Ser Val Ile Val Asn Val Cys Tyr Asp Phe
 180 185 190

tct ttg aac aat ttg tca ata tct cct tac ata tgt gga gga gca ggg 624
 Ser Leu Asn Asn Leu Ser Ile Ser Pro Tyr Ile Cys Gly Gly Ala Gly
 195 200 205

gta gat gct ata gaa ttc ttc gat gta tta cac att aag ttt gca tat 672
 Val Asp Ala Ile Glu Phe Phe Asp Val Leu His Ile Lys Phe Ala Tyr
 210 215 220

caa agc aag cta ggt att gct tat tct cta cca tct aac att agt ctc 720
 Gln Ser Lys Leu Gly Ile Ala Tyr Ser Leu Pro Ser Asn Ile Ser Leu
 225 230 235 240

ttt gct agt tta tat tac cat aaa gta atg ggc aat caa ttt aaa aat 768
 Phe Ala Ser Leu Tyr Tyr His Lys Val Met Gly Asn Gln Phe Lys Asn
 245 250 255

tta aat gtc caa gat gtt gct gaa ctt gca agt ata cct aaa att aca 816
 Leu Asn Val Gln Asp Val Ala Glu Leu Ala Ser Ile Pro Lys Ile Thr
 260 265 270

tcc gca gtt gct aca ctt aat att ggt tat ttt gga ggt gaa att ggt 864
 Ser Ala Val Ala Thr Leu Asn Ile Gly Tyr Phe Gly Gly Glu Ile Gly
 275 280 285

gca aga ttg aca ttt taa 882
 Ala Arg Leu Thr Phe
 290

<210> 44

<211> 293

<212> PRT

<213> Ehrlichia canis

<400> 44

Met Asn Asn Lys Leu Lys Phe Thr Ile Ile Asn Thr Val Leu Val Cys
1 5 10 15

Leu Leu Ser Leu Pro Asn Ile Ser Ser Ser Lys Ala Ile Asn Asn Asn
20 25 30

Ala Lys Lys Tyr Tyr Gly Leu Tyr Ile Ser Gly Gln Tyr Lys Pro Ser
35 40 45

Val Ser Val Phe Ser Asn Phe Ser Val Lys Glu Thr Asn Val Ile Thr
50 55 60

Lys Asn Leu Ile Ala Leu Lys Lys Asp Val Asp Ser Ile Glu Thr Lys
65 70 75 80

Thr Asp Ala Ser Val Gly Ile Ser Asn Pro Ser Asn Phe Thr Ile Pro
85 90 95

Tyr Thr Ala Val Phe Gln Asp Asn Ser Val Asn Phe Asn Gly Thr Ile
100 105 110

Gly Tyr Thr Phe Ala Glu Gly Thr Arg Val Glu Ile Glu Gly Ser Tyr
115 120 125

Glu Glu Phe Asp Val Lys Asn Pro Gly Gly Tyr Thr Leu Ser Asp Ala
130 135 140

Tyr Arg Tyr Phe Ala Leu Ala Arg Glu Met Lys Gly Asn Ser Phe Thr
145 150 155 160

Pro Lys Glu Lys Val Ser Asn Ser Phe Phe His Thr Val Met Arg Asn
165 170 175

Asp Gly Leu Ser Ile Ile Ser Val Ile Val Asn Val Cys Tyr Asp Phe
180 185 190

Ser Leu Asn Asn Leu Ser Ile Ser Pro Tyr Ile Cys Gly Gly Ala Gly
195 200 205

Val Asp Ala Ile Glu Phe Phe Asp Val Leu His Ile Lys Phe Ala Tyr
210 215 220

Gln Ser Lys Leu Gly Ile Ala Tyr Ser Leu Pro Ser Asn Ile Ser Leu
225 230 235 240

Phe Ala Ser Leu Tyr Tyr His Lys Val Met Gly Asn Gln Phe Lys Asn

245 250 255
 Leu Asn Val Gln Asp Val Ala Glu Leu Ala Ser Ile Pro Lys Ile Thr
 260 265 270
 Ser Ala Val Ala Thr Leu Asn Ile Gly Tyr Phe Gly Gly Glu Ile Gly
 275 280 285
 Ala Arg Leu Thr Phe
 290

<210> 45
 <211> 900
 <212> DNA
 <213> Ehrlichia canis

<220>
 <221> CDS
 <222> (1)..(900)

<400> 45
 atg aat agc aag agt aag ttc ttt aca ata tgt aca tcg tta ata tgc 48
 Met Asn Ser Lys Ser Lys Phe Phe Thr Ile Cys Thr Ser Leu Ile Cys
 1 5 10 15
 tta tta tca tca cct aac aca tct ctc tca aac ttc ata ggc aat agt 96
 Leu Leu Ser Ser Pro Asn Thr Ser Leu Ser Asn Phe Ile Gly Asn Ser
 20 25 30
 aca aaa cat tct gga tta tat gtt agc gga cat tat aag ccc agc gtt 144
 Thr Lys His Ser Gly Leu Tyr Val Ser Gly His Tyr Lys Pro Ser Val
 35 40 45
 tcc att ttt agc aaa ttt tca gta aaa gaa aca aat aca cat aca gta 192
 Ser Ile Phe Ser Lys Phe Ser Val Lys Glu Thr Asn Thr His Thr Val
 50 55 60
 cag tta gta gct ctt aaa aaa gat gtt aat tct att tct atg aac atc 240
 Gln Leu Val Ala Leu Lys Lys Asp Val Asn Ser Ile Ser Met Asn Ile
 65 70 75 80
 agt aat ggt gct aca ggc att agc aaa gca aca aat ttt aat ctt cct 288
 Ser Asn Gly Ala Thr Gly Ile Ser Lys Ala Thr Asn Phe Asn Leu Pro
 85 90 95
 tat gtt gca gaa ttt caa gac aat gcc ttc aac ttc agt gga gct att 336
 Tyr Val Ala Glu Phe Gln Asp Asn Ala Phe Asn Phe Ser Gly Ala Ile

100	105	110	
ggt tat tca ctt ttt gaa caa cta aac att gaa gtt gaa ggt tct tat			384
Gly Tyr Ser Leu Phe Glu Gln Leu Asn Ile Glu Val Glu Gly Ser Tyr			
115	120	125	
gaa gaa ttc gat gcc aaa aat cct ggt ggt tat att tta aat gat gca			432
Glu Glu Phe Asp Ala Lys Asn Pro Gly Gly Tyr Ile Leu Asn Asp Ala			
130	135	140	
ttc cgc tat ttt gca ttg gca cgt gaa atg gga caa gaa aaa aat gat			480
Phe Arg Tyr Phe Ala Leu Ala Arg Glu Met Gly Gln Glu Lys Asn Asp			
145	150	155	160
aat aag cat ctt agt cct aag gag gag cat gat ata agt aaa aca tat			528
Asn Lys His Leu Ser Pro Lys Glu Glu His Asp Ile Ser Lys Thr Tyr			
165	170	175	
tac aca gtc atg aga aat aat ggg tta tct ata tta tct att atg ata			576
Tyr Thr Val Met Arg Asn Asn Gly Leu Ser Ile Leu Ser Ile Met Ile			
180	185	190	
aat ggc tgc tat aat cta cct ctc aat gat tta tca ata tca cct tat			624
Asn Gly Cys Tyr Asn Leu Pro Leu Asn Asp Leu Ser Ile Ser Pro Tyr			
195	200	205	
ttt tgt aca gga ata ggt gta gat gct ata gaa ttt ttt gat gca ctg			672
Phe Cys Thr Gly Ile Gly Val Asp Ala Ile Glu Phe Phe Asp Ala Leu			
210	215	220	
cat ctt aaa ctt gct ttg caa agt aaa ata gga gct act tac caa tta			720
His Leu Lys Leu Ala Leu Gln Ser Lys Ile Gly Ala Thr Tyr Gln Leu			
225	230	235	240
tca gac aac att agt tta ttt aca aat gga tat tac cat caa gta ata			768
Ser Asp Asn Ile Ser Leu Phe Thr Asn Gly Tyr Tyr His Gln Val Ile			
245	250	255	
ggt gat caa ttt aaa aac tta aaa gtc caa tat ata ggt gaa ctt aaa			816
Gly Asp Gln Phe Lys Asn Leu Lys Val Gln Tyr Ile Gly Glu Leu Lys			
260	265	270	
gag aac ccg aaa att aca tct gca gtt gct act ctc aat gtt gga tac			864
Glu Asn Pro Lys Ile Thr Ser Ala Val Ala Thr Leu Asn Val Gly Tyr			
275	280	285	
ttt gga ggt gaa att gga gta aga ctc aca ctt taa			900
Phe Gly Gly Glu Ile Gly Val Arg Leu Thr Leu			

290

295

300

<210> 46

<211> 299

<212> PRT

<213> Ehrlichia canis

<400> 46

Met Asn Ser Lys Ser Lys Phe Phe Thr Ile Cys Thr Ser Leu Ile Cys
 1 5 10 15

Leu Leu Ser Ser Pro Asn Thr Ser Leu Ser Asn Phe Ile Gly Asn Ser
 20 25 30

Thr Lys His Ser Gly Leu Tyr Val Ser Gly His Tyr Lys Pro Ser Val
 35 40 45

Ser Ile Phe Ser Lys Phe Ser Val Lys Glu Thr Asn Thr His Thr Val
 50 55 60

Gln Leu Val Ala Leu Lys Lys Asp Val Asn Ser Ile Ser Met Asn Ile
 65 70 75 80

Ser Asn Gly Ala Thr Gly Ile Ser Lys Ala Thr Asn Phe Asn Leu Pro
 85 90 95

Tyr Val Ala Glu Phe Gln Asp Asn Ala Phe Asn Phe Ser Gly Ala Ile
 100 105 110

Gly Tyr Ser Leu Phe Glu Gln Leu Asn Ile Glu Val Glu Gly Ser Tyr
 115 120 125

Glu Glu Phe Asp Ala Lys Asn Pro Gly Gly Tyr Ile Leu Asn Asp Ala
 130 135 140

Phe Arg Tyr Phe Ala Leu Ala Arg Glu Met Gly Gln Glu Lys Asn Asp
 145 150 155 160

Asn Lys His Leu Ser Pro Lys Glu Glu His Asp Ile Ser Lys Thr Tyr
 165 170 175

Tyr Thr Val Met Arg Asn Asn Gly Leu Ser Ile Leu Ser Ile Met Ile
 180 185 190

Asn Gly Cys Tyr Asn Leu Pro Leu Asn Asp Leu Ser Ile Ser Pro Tyr
 195 200 205

Phe Cys Thr Gly Ile Gly Val Asp Ala Ile Glu Phe Phe Asp Ala Leu
 210 215 220

His Leu Lys Leu Ala Leu Gln Ser Lys Ile Gly Ala Thr Tyr Gln Leu
 225 230 235 240

Ser Asp Asn Ile Ser Leu Phe Thr Asn Gly Tyr Tyr His Gln Val Ile
 245 250 255

Gly Asp Gln Phe Lys Asn Leu Lys Val Gln Tyr Ile Gly Glu Leu Lys
 260 265 270

Glu Asn Pro Lys Ile Thr Ser Ala Val Ala Thr Leu Asn Val Gly Tyr
 275 280 285

Phe Gly Gly Glu Ile Gly Val Arg Leu Thr Leu
 290 295

<210> 47

<211> 843

<212> DNA

<213> Ehrlichia canis

<220>

<221> CDS

<222> (1)..(843)

<400> 47

atg aat tat aag aaa att cta gta aga agc gcg tta atc tca tta atg 48
 Met Asn Tyr Lys Lys Ile Leu Val Arg Ser Ala Leu Ile Ser Leu Met
 1 5 10 15

tca atc tta cca tat cag tct ttt gca gat cct gta ggt tca aga act 96
 Ser Ile Leu Pro Tyr Gln Ser Phe Ala Asp Pro Val Gly Ser Arg Thr
 20 25 30

aat gat aac aaa gaa ggc ttc tac att agt gca aag tac aat cca agt 144
 Asn Asp Asn Lys Glu Gly Phe Tyr Ile Ser Ala Lys Tyr Asn Pro Ser
 35 40 45

ata tca cac ttt aga aaa ttc tct gct gaa gaa act cct att aat gga 192
 Ile Ser His Phe Arg Lys Phe Ser Ala Glu Glu Thr Pro Ile Asn Gly
 50 55 60

aca aat tct ctc act aaa aaa gtt ttc gga cta aag aaa gat ggt gat 240
 Thr Asn Ser Leu Thr Lys Lys Val Phe Gly Leu Lys Lys Asp Gly Asp
 65 70 75 80

ata aca aaa aaa gac gat ttt aca aga gta gct cca ggc att gat ttt	288
Ile Thr Lys Lys Asp Asp Phe Thr Arg Val Ala Pro Gly Ile Asp Phe	
85 90 95	
caa aat aac tta ata tca gga ttt tca gga agt att ggt tac tct atg	336
Gln Asn Asn Leu Ile Ser Gly Phe Ser Gly Ser Ile Gly Tyr Ser Met	
100 105 110	
gac gga cca aga ata gaa ctt gaa gct gca tat caa caa ttt aat cca	384
Asp Gly Pro Arg Ile Glu Leu Glu Ala Ala Tyr Gln Gln Phe Asn Pro	
115 120 125	
aaa aac acc gat aac aat gat act gat aat ggt gaa tac tat aaa cat	432
Lys Asn Thr Asp Asn Asn Asp Thr Asp Asn Gly Glu Tyr Tyr Lys His	
130 135 140	
ttt gca tta tct cgt aaa gat gca atg gaa gat cag caa tat gta gta	480
Phe Ala Leu Ser Arg Lys Asp Ala Met Glu Asp Gln Gln Tyr Val Val	
145 150 155 160	
ctt aaa aat gac ggc ata act ttt atg tca ttg atg gtt aat act tgc	528
Leu Lys Asn Asp Gly Ile Thr Phe Met Ser Leu Met Val Asn Thr Cys	
165 170 175	
tat gac att aca gct gaa gga gta tct ttc gta cca tat gca tgt gca	576
Tyr Asp Ile Thr Ala Glu Gly Val Ser Phe Val Pro Tyr Ala Cys Ala	
180 185 190	
ggt ata gga gca gat ctt atc act att ttt aaa gac ctc aat cta aaa	624
Gly Ile Gly Ala Asp Leu Ile Thr Ile Phe Lys Asp Leu Asn Leu Lys	
195 200 205	
ttt gct tac caa gga aaa ata ggt att agt tac cct atc aca cca gaa	672
Phe Ala Tyr Gln Gly Lys Ile Gly Ile Ser Tyr Pro Ile Thr Pro Glu	
210 215 220	
gtc tct gca ttt att ggt gga tac tac cat ggc gtt att ggt aat aaa	720
Val Ser Ala Phe Ile Gly Gly Tyr Tyr His Gly Val Ile Gly Asn Lys	
225 230 235 240	
ttt gag aag ata cct gta ata act cct gta gta tta aat gat gct cct	768
Phe Glu Lys Ile Pro Val Ile Thr Pro Val Val Leu Asn Asp Ala Pro	
245 250 255	
caa acc aca tct gct tca gta act ctt gac gtt gga tac ttt ggc gga	816
Gln Thr Thr Ser Ala Ser Val Thr Leu Asp Val Gly Tyr Phe Gly Gly	
260 265 270	

gaa att gga atg agg ttc acc ttc taa
 Glu Ile Gly Met Arg Phe Thr Phe
 275 280

843

<210> 48
 <211> 280
 <212> PRT
 <213> Ehrlichia canis

<400> 48
 Met Asn Tyr Lys Lys Ile Leu Val Arg Ser Ala Leu Ile Ser Leu Met
 1 5 10 15

Ser Ile Leu Pro Tyr Gln Ser Phe Ala Asp Pro Val Gly Ser Arg Thr
 20 25 30

Asn Asp Asn Lys Glu Gly Phe Tyr Ile Ser Ala Lys Tyr Asn Pro Ser
 35 40 45

Ile Ser His Phe Arg Lys Phe Ser Ala Glu Glu Thr Pro Ile Asn Gly
 50 55 60

Thr Asn Ser Leu Thr Lys Lys Val Phe Gly Leu Lys Lys Asp Gly Asp
 65 70 75 80

Ile Thr Lys Lys Asp Asp Phe Thr Arg Val Ala Pro Gly Ile Asp Phe
 85 90 95

Gln Asn Asn Leu Ile Ser Gly Phe Ser Gly Ser Ile Gly Tyr Ser Met
 100 105 110

Asp Gly Pro Arg Ile Glu Leu Glu Ala Ala Tyr Gln Gln Phe Asn Pro
 115 120 125

Lys Asn Thr Asp Asn Asn Asp Thr Asp Asn Gly Glu Tyr Tyr Lys His
 130 135 140

Phe Ala Leu Ser Arg Lys Asp Ala Met Glu Asp Gln Gln Tyr Val Val
 145 150 155 160

Leu Lys Asn Asp Gly Ile Thr Phe Met Ser Leu Met Val Asn Thr Cys
 165 170 175

Tyr Asp Ile Thr Ala Glu Gly Val Ser Phe Val Pro Tyr Ala Cys Ala
 180 185 190

Gly Ile Gly Ala Asp Leu Ile Thr Ile Phe Lys Asp Leu Asn Leu Lys
 195 200 205

Phe Ala Tyr Gln Gly Lys Ile Gly Ile Ser Tyr Pro Ile Thr Pro Glu
 210 215 220

Val Ser Ala Phe Ile Gly Gly Tyr Tyr His Gly Val Ile Gly Asn Lys
 225 230 235 240

Phe Glu Lys Ile Pro Val Ile Thr Pro Val Val Leu Asn Asp Ala Pro
 245 250 255

Gln Thr Thr Ser Ala Ser Val Thr Leu Asp Val Gly Tyr Phe Gly Gly
 260 265 270

Glu Ile Gly Met Arg Phe Thr Phe
 275 280

<210> 49

<211> 903

<212> DNA

<213> OMP-12

<220>

<221> CDS

<222> (1)..(903)

<400> 49

atg aag aag aaa aat caa ttt atc aca ata agt aca ata tta gta tgt 48
 Met Lys Lys Lys Asn Gln Phe Ile Thr Ile Ser Thr Ile Leu Val Cys
 1 5 10 15

tta ttg tca tta tct aat gca tca ctt tca aac act aca aat agc agc 96
 Leu Leu Ser Leu Ser Asn Ala Ser Leu Ser Asn Thr Thr Asn Ser Ser
 20 25 30

act aaa aaa cag ttt ggg tta tat gtt agt gga caa tac aag cct agt 144
 Thr Lys Lys Gln Phe Gly Leu Tyr Val Ser Gly Gln Tyr Lys Pro Ser
 35 40 45

gtt tct att ttt agc aat ttc tca gta aag gaa act aat ttt cct aca 192
 Val Ser Ile Phe Ser Asn Phe Ser Val Lys Glu Thr Asn Phe Pro Thr
 50 55 60

aag tat cta gca gct ctt aaa aaa gac att aat tct gtc gaa ttt gac 240
 Lys Tyr Leu Ala Ala Leu Lys Lys Asp Ile Asn Ser Val Glu Phe Asp
 65 70 75 80

gat agt gtt act gct ggc att agt tac cca ctt aat ttc agt act cct	288
Asp Ser Val Thr Ala Gly Ile Ser Tyr Pro Leu Asn Phe Ser Thr Pro	
85 90 95	
tat ata gct gta ttt caa gat aat att tct aat ttt aat ggc gct att	336
Tyr Ile Ala Val Phe Gln Asp Asn Ile Ser Asn Phe Asn Gly Ala Ile	
100 105 110	
ggg tac act ttt gtt gaa ggc cca aga att gaa ata gaa ggt tct tat	384
Gly Tyr Thr Phe Val Glu Gly Pro Arg Ile Glu Ile Glu Gly Ser Tyr	
115 120 125	
gaa gaa ttc gat gtc aaa gac ctg gaa gat ata cag aaa tac aag atg	432
Glu Glu Phe Asp Val Lys Asp Leu Glu Asp Ile Gln Lys Tyr Lys Met	
130 135 140	
cat acc gtt gac ttt gct tta gca cgt gat ata gac tct att cct act	480
His Thr Val Asp Phe Ala Leu Ala Arg Asp Ile Asp Ser Ile Pro Thr	
145 150 155 160	
agc cca aaa aat aga act tca cat gat ggc aac agt tca tat aag gta	528
Ser Pro Lys Asn Arg Thr Ser His Asp Gly Asn Ser Ser Tyr Lys Val	
165 170 175	
tac cac act gta atg aaa aat gaa gga cta tct ata ata tcc att atg	576
Tyr His Thr Val Met Lys Asn Glu Gly Leu Ser Ile Ile Ser Ile Met	
180 185 190	
gtc aat ggc tgc tat gat ttt tct tca gat aat tta tca ata tta cct	624
Val Asn Gly Cys Tyr Asp Phe Ser Ser Asp Asn Leu Ser Ile Leu Pro	
195 200 205	
tat gta tgt ggt ggt ata ggt gta aat gct ata gag ttt ttc gat gca	672
Tyr Val Cys Gly Gly Ile Gly Val Asn Ala Ile Glu Phe Phe Asp Ala	
210 215 220	
tta cat gtt aaa ttc gcg tgt cag ggt aaa tta ggt att act tat cca	720
Leu His Val Lys Phe Ala Cys Gln Gly Lys Leu Gly Ile Thr Tyr Pro	
225 230 235 240	
tta tct tcc aac gtt agt tta ttt gct ggt gga tat tat cac caa gta	768
Leu Ser Ser Asn Val Ser Leu Phe Ala Gly Gly Tyr Tyr His Gln Val	
245 250 255	
atg ggc aac caa ttt aaa aat cta aat gtt caa cat gta gct gaa ctt	816
Met Gly Asn Gln Phe Lys Asn Leu Asn Val Gln His Val Ala Glu Leu	
260 265 270	

aat gac gca ccc aaa gtt aca tct gca gta gct aca ctt gac att ggg 864
 Asn Asp Ala Pro Lys Val Thr Ser Ala Val Ala Thr Leu Asp Ile Gly
 275 280 285

tat ttt ggt ggt gaa att gga gca agg ctt ata ttt taa 903
 Tyr Phe Gly Gly Glu Ile Gly Ala Arg Leu Ile Phe
 290 295 300

<210> 50
 <211> 300
 <212> PRT
 <213> OMP-1Z

<400> 50
 Met Lys Lys Lys Asn Gln Phe Ile Thr Ile Ser Thr Ile Leu Val Cys
 1 5 10 15

Leu Leu Ser Leu Ser Asn Ala Ser Leu Ser Asn Thr Thr Asn Ser Ser
 20 25 30

Thr Lys Lys Gln Phe Gly Leu Tyr Val Ser Gly Gln Tyr Lys Pro Ser
 35 40 45

Val Ser Ile Phe Ser Asn Phe Ser Val Lys Glu Thr Asn Phe Pro Thr
 50 55 60

Lys Tyr Leu Ala Ala Leu Lys Lys Asp Ile Asn-Ser Val Glu Phe Asp
 65 70 75 80

Asp Ser Val Thr Ala Gly Ile Ser Tyr Pro Leu Asn Phe Ser Thr Pro
 85 90 95

Tyr Ile Ala Val Phe Gln Asp Asn Ile Ser Asn Phe Asn Gly Ala Ile
 100 105 110

Gly Tyr Thr Phe Val Glu Gly Pro Arg Ile Glu Ile Glu Gly Ser Tyr
 115 120 125

Glu Glu Phe Asp Val Lys Asp Leu Glu Asp Ile Gln Lys Tyr Lys Met
 130 135 140

His Thr Val Asp Phe Ala Leu Ala Arg Asp Ile Asp Ser Ile Pro Thr
 145 150 155 160

Ser Pro Lys Asn Arg Thr Ser His Asp Gly Asn Ser Ser Tyr Lys Val
 165 170 175

Tyr His Thr Val Met Lys Asn Glu Gly Leu Ser Ile Ile Ser Ile Met
180 185 190

Val Asn Gly Cys Tyr Asp Phe Ser Ser Asp Asn Leu Ser Ile Leu Pro
195 200 205

Tyr Val Cys Gly Gly Ile Gly Val Asn Ala Ile Glu Phe Phe Asp Ala
210 215 220

Leu His Val Lys Phe Ala Cys Gln Gly Lys Leu Gly Ile Thr Tyr Pro
225 230 235 240

Leu Ser Ser Asn Val Ser Leu Phe Ala Gly Gly Tyr Tyr His Gln Val
245 250 255

Met Gly Asn Gln Phe Lys Asn Leu Asn Val Gln His Val Ala Glu Leu
260 265 270

Asn Asp Ala Pro Lys Val Thr Ser Ala Val Ala Thr Leu Asp Ile Gly
275 280 285

Tyr Phe Gly Gly Glu Ile Gly Ala Arg Leu Ile Phe
290 295 300

<210> 51

<211> 897

<212> DNA

<213> OMP-1H

<220>

<221> CDS

<222> (1)..(897)

<400> 51

atg aat cac aaa agt atg ctc ttt aca ata ggt aca gct ttg ata tcc 48
Met Asn His Lys Ser Met Leu Phe Thr Ile Gly Thr Ala Leu Ile Ser
1 5 10 15

tta ttg tca tta cct aat gta tca ttc tca gga atc ata aat aac aat 96
Leu Leu Ser Leu Pro Asn Val Ser Phe Ser Gly Ile Ile Asn Asn Asn
20 25 30

gct aac aat tta ggt ata tac att agt ggg caa tat aaa ccc agt gtt 144
Ala Asn Asn Leu Gly Ile Tyr Ile Ser Gly Gln Tyr Lys Pro Ser Val
35 40 45

tct gtt ttt agc aat ttc tca gta aaa gaa act aac ttc act aca caa	192
Ser Val Phe Ser Asn Phe Ser Val Lys Glu Thr Asn Phe Thr Thr Gln	
50 55 60	
cag tta gta gca ctt aaa aaa gat att gat tct gtt gac att agt acc	240
Gln Leu Val Ala Leu Lys Lys Asp Ile Asp Ser Val Asp Ile Ser Thr	
65 70 75 80	
aat gct gat agc ggt att aat aat ccg cag aat ttc act atc cct tat	288
Asn Ala Asp Ser Gly Ile Asn Asn Pro Gln Asn Phe Thr Ile Pro Tyr	
85 90 95	
ata cca aaa ttt caa gac aat gct gct agt ttt agt gga gca ctt gga	336
Ile Pro Lys Phe Gln Asp Asn Ala Ala Ser Phe Ser Gly Ala Leu Gly	
100 105 110	
ttc ttc tac gct aga ggt tta aga ctt gaa atg gaa ggt tcc tat gaa	384
Phe Phe Tyr Ala Arg Gly Leu Arg Leu Glu Met Glu Gly Ser Tyr Glu	
115 120 125	
gaa ttt gat gtt aaa aac cct gga gga tat aca aaa gta aaa gat gca	432
Glu Phe Asp Val Lys Asn Pro Gly Gly Tyr Thr Lys Val Lys Asp Ala	
130 135 140	
tat cgt tac ttt gcc ctg gca cgt gag atg caa tct ggt caa act tgc	480
Tyr Arg Tyr Phe Ala Leu Ala Arg Glu Met Gln Ser Gly Gln Thr Cys	
145 150 155 160	
cct aaa cac aaa gaa aca tca ggt att caa cct cac ggt att tat cac	528
Pro Lys His Lys Glu Thr Ser Gly Ile Gln Pro His Gly Ile Tyr His	
165 170 175	
act gtt atg agg aat gat ggg gta tct att tca tct gtc ata atc aat	576
Thr Val Met Arg Asn Asp Gly Val Ser Ile Ser Ser Val Ile Ile Asn	
180 185 190	
ggt tgt tat aac ttt act tta agt aat cta cca ata tca cct tac atg	624
Gly Cys Tyr Asn Phe Thr Leu Ser Asn Leu Pro Ile Ser Pro Tyr Met	
195 200 205	
tgt gta ggt atg gga ata gat gct ata caa ttt ttt gat tca cta cat	672
Cys Val Gly Met Gly Ile Asp Ala Ile Gln Phe Phe Asp Ser Leu His	
210 215 220	
att aag ttt gca cat caa agt aag tta ggt att act tac cca cta tct	720
Ile Lys Phe Ala His Gln Ser Lys Leu Gly Ile Thr Tyr Pro Leu Ser	
225 230 235 240	

tca aat gtt cat tta ttt gct gat agc tat tat cat aaa gta ata ggt 768
 Ser Asn Val His Leu Phe Ala Asp Ser Tyr Tyr His Lys Val Ile Gly
 245 250 255

aat aaa ttt aaa aat cta agg gtt caa cac gtt tat gaa tta caa cag 816
 Asn Lys Phe Lys Asn Leu Arg Val Gln His Val Tyr Glu Leu Gln Gln
 260 265 270

gta cct aaa gtt aca tct gct gtt gct aca ctt gat att ggg tat ttt 864
 Val Pro Lys Val Thr Ser Ala Val Ala Thr Leu Asp Ile Gly Tyr Phe
 275 280 285

ggt ggt gaa gtt gga gta agg ttt ata ctt taa 897
 Gly Gly Glu Val Gly Val Arg Phe Ile Leu
 290 295

<210> 52
 <211> 298
 <212> PRT
 <213> OMP-1H

<400> 52
 Met Asn His Lys Ser Met Leu Phe Thr Ile Gly Thr Ala Leu Ile Ser
 1 5 10 15

Leu Leu Ser Leu Pro Asn Val Ser Phe Ser Gly Ile Ile Asn Asn Asn
 20 25 30

Ala Asn Asn Leu Gly Ile Tyr Ile Ser Gly Gln Tyr Lys Pro Ser Val
 35 40 45

Ser Val Phe Ser Asn Phe Ser Val Lys Glu Thr Asn Phe Thr Thr Gln
 50 55 60

Gln Leu Val Ala Leu Lys Lys Asp Ile Asp Ser Val Asp Ile Ser Thr
 65 70 75 80

Asn Ala Asp Ser Gly Ile Asn Asn Pro Gln Asn Phe Thr Ile Pro Tyr
 85 90 95

Ile Pro Lys Phe Gln Asp Asn Ala Ala Ser Phe Ser Gly Ala Leu Gly
 100 105 110

Phe Phe Tyr Ala Arg Gly Leu Arg Leu Glu Met Glu Gly Ser Tyr Glu
 115 120 125

Glu Phe Asp Val Lys Asn Pro Gly Gly Tyr Thr Lys Val Lys Asp Ala

130 135 140
 Tyr Arg Tyr Phe Ala Leu Ala Arg Glu Met Gln Ser Gly Gln Thr Cys
 145 150 155 160
 Pro Lys His Lys Glu Thr Ser Gly Ile Gln Pro His Gly Ile Tyr His
 165 170 175
 Thr Val Met Arg Asn Asp Gly Val Ser Ile Ser Ser Val Ile Ile Asn
 180 185 190
 Gly Cys Tyr Asn Phe Thr Leu Ser Asn Leu Pro Ile Ser Pro Tyr Met
 195 200 205
 Cys Val Gly Met Gly Ile Asp Ala Ile Gln Phe Phe Asp Ser Leu His
 210 215 220
 Ile Lys Phe Ala His Gln Ser Lys Leu Gly Ile Thr Tyr Pro Leu Ser
 225 230 235 240
 Ser Asn Val His Leu Phe Ala Asp Ser Tyr Tyr His Lys Val Ile Gly
 245 250 255
 Asn Lys Phe Lys Asn Leu Arg Val Gln His Val Tyr Glu Leu Gln
 260 265 270
 Val Pro Lys Val Thr Ser Ala Val Ala Thr Leu Asp Ile Gly Tyr Phe
 275 280 285
 Gly Gly Glu Val Gly Val Arg Phe Ile Leu
 290 295

<210> 53
 <211> 882
 <212> DNA
 <213> p30-6

<220>
 <221> CDS
 <222> (1)..(882)

<400> 53
 atg gca aat ttt atg tac aaa aaa tac aaa cta atg aca gca ggt gta 48
 Met Ala Asn Phe Met Tyr Lys Lys Tyr Lys Leu Met Thr Ala Gly Val
 1 5 10 15
 gta tta ttt cac atg tta ttt cta cct cat gtt tct ttc gca aaa aat 96

Val	Leu	Phe	His	Met	Leu	Phe	Leu	Pro	His	Val	Ser	Phe	Ala	Lys	Asn			
				20					25					30				
aca	aac	agc	aat	aaa	ctt	gga	tta	tac	atc	agt	gga	cag	tat	aac	cct	144		
Thr	Asn	Ser	Asn	Lys	Leu	Gly	Leu	Tyr	Ile	Ser	Gly	Gln	Tyr	Asn	Pro			
				35					40					45				
agt	gtt	tct	gtt	ttt	agc	aat	ttt	tca	gca	aaa	gaa	acc	aat	gtt	cat	192		
Ser	Val	Ser	Val	Phe	Ser	Asn	Phe	Ser	Ala	Lys	Glu	Thr	Asn	Val	His			
				50					55					60				
aca	gta	caa	ctc	atg	gcg	ctt	aaa	aaa	gac	att	gat	tct	att	gaa	gtt	240		
Thr	Val	Gln	Leu	Met	Ala	Leu	Lys	Lys	Asp	Ile	Asp	Ser	Ile	Glu	Val			
				65					70					75				
gat	act	gga	aat	agc	gca	ggg	att	agc	aaa	cca	caa	aat	ttc	aca	gtt	288		
Asp	Thr	Gly	Asn	Ser	Ala	Gly	Ile	Ser	Lys	Pro	Gln	Asn	Phe	Thr	Val			
				85					90					95				
ctt	tat	act	cca	aaa	ttt	caa	gat	aat	gtt	gct	ggg	ctt	agc	ggg	gca	336		
Leu	Tyr	Thr	Pro	Lys	Phe	Gln	Asp	Asn	Val	Ala	Gly	Leu	Ser	Gly	Ala			
				100					105					110				
ctt	gga	ttc	ttt	tat	tct	aaa	gga	tta	agg	att	gaa	atg	ggg	ttt	tct	384		
Leu	Gly	Phe	Phe	Tyr	Ser	Lys	Gly	Leu	Arg	Ile	Glu	Met	Gly	Phe	Ser			
				115					120					125				
tat	gaa	aaa	ttt	gat	gct	aaa	gac	ctt	ggg	gag	tac	acc	aaa	ata	aaa	432		
Tyr	Glu	Lys	Phe	Asp	Ala	Lys	Asp	Leu	Gly	Glu	Tyr	Thr	Lys	Ile	Lys			
				130					135					140				
gat	gct	tat	aga	tat	ttt	gct	cta	gta	cgt	gaa	atg	cat	gtt	agt	ctc	480		
Asp	Ala	Tyr	Arg	Tyr	Phe	Ala	Leu	Val	Arg	Glu	Met	His	Val	Ser	Leu			
				145					150					155				
att	tat	cca	aaa	gat	aat	aac	aca	gga	aca	cat	tat	act	gtt	atg	aga	528		
Ile	Tyr	Pro	Lys	Asp	Asn	Asn	Thr	Gly	Thr	His	Tyr	Thr	Val	Met	Arg			
				165					170					175				
aat	gat	ggg	ata	tct	att	tct	tct	gct	aca	gta	aat	ggc	tgc	tat	gat	576		
Asn	Asp	Gly	Ile	Ser	Ile	Ser	Ser	Ala	Thr	Val	Asn	Gly	Cys	Tyr	Asp			
				180					185					190				
tct	ttt	ttc	cag	ttt	atc	ttt	gtc	acc	tat	atg	tgt	ata	ggc	atc	ggg	624		
Ser	Phe	Phe	Gln	Phe	Ile	Phe	Val	Thr	Tyr	Met	Cys	Ile	Gly	Ile	Gly			
				195					200					205				
ata	gat	gct	ata	gaa	ttt	ctt	aat	gca	tac	ata	tta	agt	ttg	ctt	gcc	672		

Ile Asp Ala Ile Glu Phe Leu Asn Ala Tyr Ile Leu Ser Leu Leu Ala
 210 215 220

aag gta gtt aag gtg tta act tat tct gta tct ccc aat gtt aat tta 720
 Lys Val Val Lys Val Leu Thr Tyr Ser Val Ser Pro Asn Val Asn Leu
 225 230 235 240

ttt gca gat gga tat tat cat aaa gtg atg ggc aat aaa ttt aaa aat 768
 Phe Ala Asp Gly Tyr Tyr His Lys Val Met Gly Asn Lys Phe Lys Asn
 245 250 255

tta cct gtt caa tac gtt aat act tta gaa gag tat cca aga gtt aca 816
 Leu Pro Val Gln Tyr Val Asn Thr Leu Glu Glu Tyr Pro Arg Val Thr
 260 265 270

tct gca att gct aca ctt gat att ggc tac ctc ggt ggt gaa att ggc 864
 Ser Ala Ile Ala Thr Leu Asp Ile Gly Tyr Leu Gly Gly Glu Ile Gly
 275 280 285

ata aga ttt ata ttt taa 882
 Ile Arg Phe Ile Phe
 290

<210> 54
 <211> 293
 <212> PRT
 <213> p30-6

<400> 54
 Met Ala Asn Phe Met Tyr Lys Lys Tyr Lys Leu Met Thr Ala Gly Val
 1 5 10 15

Val Leu Phe His Met Leu Phe Leu Pro His Val Ser Phe Ala Lys Asn
 20 25 30

Thr Asn Ser Asn Lys Leu Gly Leu Tyr Ile Ser Gly Gln Tyr Asn Pro
 35 40 45

Ser Val Ser Val Phe Ser Asn Phe Ser Ala Lys Glu Thr Asn Val His
 50 55 60

Thr Val Gln Leu Met Ala Leu Lys Lys Asp Ile Asp Ser Ile Glu Val
 65 70 75 80

Asp Thr Gly Asn Ser Ala Gly Ile Ser Lys Pro Gln Asn Phe Thr Val
 85 90 95

Leu Tyr Thr Pro Lys Phe Gln Asp Asn Val Ala Gly Leu Ser Gly Ala
100 105 110

Leu Gly Phe Phe Tyr Ser Lys Gly Leu Arg Ile Glu Met Gly Phe Ser
115 120 125

Tyr Glu Lys Phe Asp Ala Lys Asp Leu Gly Glu Tyr Thr Lys Ile Lys
130 135 140

Asp Ala Tyr Arg Tyr Phe Ala Leu Val Arg Glu Met His Val Ser Leu
145 150 155 160

Ile Tyr Pro Lys Asp Asn Asn Thr Gly Thr His Tyr Thr Val Met Arg
165 170 175

Asn Asp Gly Ile Ser Ile Ser Ser Ala Thr Val Asn Gly Cys Tyr Asp
180 185 190

Ser Phe Phe Gln Phe Ile Phe Val Thr Tyr Met Cys Ile Gly Ile Gly
195 200 205

Ile Asp Ala Ile Glu Phe Leu Asn Ala Tyr Ile Leu Ser Leu Leu Ala
210 215 220

Lys Val Val Lys Val Leu Thr Tyr Ser Val Ser Pro Asn Val Asn Leu
225 230 235 240

Phe Ala Asp Gly Tyr Tyr His Lys Val Met Gly Asn Lys Phe Lys Asn
245 250 255

Leu Pro Val Gln Tyr Val Asn Thr Leu Glu Glu Tyr Pro Arg Val Thr
260 265 270

Ser Ala Ile Ala Thr Leu Asp Ile Gly Tyr Leu Gly Gly Glu Ile Gly
275 280 285

Ile Arg Phe Ile Phe
290

<210> 55

<211> 891

<212> DNA

<213> p30-7

<220>

<221> CDS

<222> (1)..(891)

<400> 55

atg gga aat tct atg aat aat aaa agt caa ttc tta ata aga ttt ata 48
Met Gly Asn Ser Met Asn Asn Lys Ser Gln Phe Leu Ile Arg Phe Ile
1 5 10 15

ttt tta aca tgc atg ctg tca tta cct aat ata tct ctt tca aaa gta 96
Phe Leu Thr Cys Met Leu Ser Leu Pro Asn Ile Ser Leu Ser Lys Val
20 25 30

aat aac gaa aaa cat tct ggt ttg tat att agc ggg caa tac aaa ccc 144
Asn Asn Glu Lys His Ser Gly Leu Tyr Ile Ser Gly Gln Tyr Lys Pro
35 40 45

agt gtt tct gtt ttc agt aat ttt tca gtt aaa gaa acc aac ttt cat 192
Ser Val Ser Val Phe Ser Asn Phe Ser Val Lys Glu Thr Asn Phe His
50 55 60

aca aaa cat ctc ata gct ctt aaa caa gat gtt gat tct gtt gaa att 240
Thr Lys His Leu Ile Ala Leu Lys Gln Asp Val Asp Ser Val Glu Ile
65 70 75 80

gat act ggt agt aat aca gca ggt att agt aac cca tct aac ttt aca 288
Asp Thr Gly Ser Asn Thr Ala Gly Ile Ser Asn Pro Ser Asn Phe Thr
85 90 95

atc cct tat act gca gaa ttt caa gac aac cat act aac tgc aat ggc 336
Ile Pro Tyr Thr Ala Glu Phe Gln Asp Asn His Thr Asn Cys Asn Gly
100 105 110

tct att ggt tat gct ttt gct gaa ggt cca aga att gaa ata gaa tta 384
Ser Ile Gly Tyr Ala Phe Ala Glu Gly Pro Arg Ile Glu Ile Glu Leu
115 120 125

tca tat gaa aaa ttt gat gtt aaa aat ccc aca ggg tat act aca gta 432
Ser Tyr Glu Lys Phe Asp Val Lys Asn Pro Thr Gly Tyr Thr Thr Val
130 135 140

aaa gat gct tat aga tac ttt gct tta gca cgt gaa ata aat att tct 480
Lys Asp Ala Tyr Arg Tyr Phe Ala Leu Ala Arg Glu Ile Asn Ile Ser
145 150 155 160

cta ttc caa cca aaa caa aaa gaa ggt agt gga att tac cat gtc gta 528
Leu Phe Gln Pro Lys Gln Lys Glu Gly Ser Gly Ile Tyr His Val Val
165 170 175

atg aaa aac gat ggg tta tct atc tta tcc aat ata gtt aat att tgc 576
Met Lys Asn Asp Gly Leu Ser Ile Leu Ser Asn Ile Val Asn Ile Cys

180

185

190

tac gat ttt tct tta aat aat tta cct ata tca cct tat tta tgc gga 624
 Tyr Asp Phe Ser Leu Asn Asn Leu Pro Ile Ser Pro Tyr Leu Cys Gly.
 195 200 205

gga atg ggt ata aat gcc ata gaa ttc ttt gac gct tta cat gtg aaa 672
 Gly Met Gly Ile Asn Ala Ile Glu Phe Phe Asp Ala Leu His Val Lys
 210 215 220

ttt gct tat caa agc aag gca gga att agt tat caa cta tta cgt aaa 720
 Phe Ala Tyr Gln Ser Lys Ala Gly Ile Ser Tyr Gln Leu Leu Arg Lys
 225 230 235 240

atc aac tta ttt att gat gta tat tac tac gaa gta ata agt aat aaa 768
 Ile Asn Leu Phe Ile Asp Val Tyr Tyr Tyr Glu Val Ile Ser Asn Lys
 245 250 255

ttt aaa aac ctg aaa gtc caa cat gta cat gaa ctt aaa gat aat cca 816
 Phe Lys Asn Leu Lys Val Gln His Val His Glu Leu Lys Asp Asn Pro
 260 265 270

aaa gtc aca tct gca gtt gct aca ctt gat ata gca tat ttt ggt agt 864
 Lys Val Thr Ser Ala Val Ala Thr Leu Asp Ile Ala Tyr Phe Gly Ser
 275 280 285

gaa gct ggc ata aga att ata ttt taa 891
 Glu Ala Gly Ile Arg Ile Ile Phe
 290 295

<210> 56

<211> 296

<212> PRT

<213> p30-7

<400> 56

Met Gly Asn Ser Met Asn Asn Lys Ser Gln Phe Leu Ile Arg Phe Ile
 1 5 10 15

Phe Leu Thr Cys Met Leu Ser Leu Pro Asn Ile Ser Leu Ser Lys Val
 20 25 30

Asn Asn Glu Lys His Ser Gly Leu Tyr Ile Ser Gly Gln Tyr Lys Pro
 35 40 45

Ser Val Ser Val Phe Ser Asn Phe Ser Val Lys Glu Thr Asn Phe His
 50 55 60

Thr Lys His Leu Ile Ala Leu Lys Gln Asp Val Asp Ser Val Glu Ile
65 70 75 80

Asp Thr Gly Ser Asn Thr Ala Gly Ile Ser Asn Pro Ser Asn Phe Thr
85 90 95

Ile Pro Tyr Thr Ala Glu Phe Gln Asp Asn His Thr Asn Cys Asn Gly
100 105 110

Ser Ile Gly Tyr Ala Phe Ala Glu Gly Pro Arg Ile Glu Ile Glu Leu
115 120 125

Ser Tyr Glu Lys Phe Asp Val Lys Asn Pro Thr Gly Tyr Thr Thr Val
130 135 140

Lys Asp Ala Tyr Arg Tyr Phe Ala Leu Ala Arg Glu Ile Asn Ile Ser
145 150 155 160

Leu Phe Gln Pro Lys Gln Lys Glu Gly Ser Gly Ile Tyr His Val Val
165 170 175

Met Lys Asn Asp Gly Leu Ser Ile Leu Ser Asn Ile Val Asn Ile Cys
180 185 190

Tyr Asp Phe Ser Leu Asn Asn Leu Pro Ile Ser Pro Tyr Leu Cys Gly
195 200 205

Gly Met Gly Ile Asn Ala Ile Glu Phe Phe Asp Ala Leu His Val Lys
210 215 220

Phe Ala Tyr Gln Ser Lys Ala Gly Ile Ser Tyr Gln Leu Leu Arg Lys
225 230 235 240

Ile Asn Leu Phe Ile Asp Val Tyr Tyr Tyr Glu Val Ile Ser Asn Lys
245 250 255

Phe Lys Asn Leu Lys Val Gln His Val His Glu Leu Lys Asp Asn Pro
260 265 270

Lys Val Thr Ser Ala Val Ala Thr Leu Asp Ile Ala Tyr Phe Gly Ser
275 280 285

Glu Ala Gly Ile Arg Ile Ile Phe
290 295

<210> 57

<211> 846
 <212> DNA
 <213> p30-9

<220>
 <221> CDS
 <222> (1)..(846)

<400> 57

atg aat aat aaa aga aat ttt ttt tta ata ggt atg tct cta ttg ata	48
Met Asn Asn Lys Arg Asn Phe Phe Leu Ile Gly Met Ser Leu Leu Ile	
1 5 10 15	
aat cta cta ttg cca att gat gcc tct tct atg gaa gta cat aat tat	96
Asn Leu Leu Leu Pro Ile Asp Ala Ser Ser Met Glu Val His Asn Tyr	
20 25 30	
aca cat ttt aca cct agg ctg tat att agt ggg caa tac agg cca gga	144
Thr His Phe Thr Pro Arg Leu Tyr Ile Ser Gly Gln Tyr Arg Pro Gly	
35 40 45	
gtt tcc cac ttt agc aaa ttt tca gtc aaa gaa aca cat tgt aat act	192
Val Ser His Phe Ser Lys Phe Ser Val Lys Glu Thr His Cys Asn Thr	
50 55 60	
gtg caa tta gtt ggg cta aca aaa gat ata aaa gta act aat aac agt	240
Val Gln Leu Val Gly Leu Thr Lys Asp Ile Lys Val Thr Asn Asn Ser	
65 70 75 80	
agt atc aac aca aat act agt ttt aac ttt cct tat gtt gca gaa ttt	288
Ser Ile Asn Thr Asn Thr Ser Phe Asn Phe Pro Tyr Val Ala Glu Phe	
85 90 95	
caa gat aac gca atg agc ttt agt gga gca ata gga tgc ttt tat tca	336
Gln Asp Asn Ala Met Ser Phe Ser Gly Ala Ile Gly Cys Phe Tyr Ser	
100 105 110	
gaa cac ttc aga att gaa gta gaa gct tct tat gaa gaa ttt gac gtt	384
Glu His Phe Arg Ile Glu Val Glu Ala Ser Tyr Glu Glu Phe Asp Val	
115 120 125	
aaa aat cct gaa gga tct act aca gac tcc tat aga tat ttc gcg tta	432
Lys Asn Pro Glu Gly Ser Thr Thr Asp Ser Tyr Arg Tyr Phe Ala Leu	
130 135 140	
gca cgt ggc atg gat ggt aat aat att cct aca agt caa aaa ttt act	480
Ala Arg Gly Met Asp Gly Asn Asn Ile Pro Thr Ser Gln Lys Phe Thr	
145 150 155 160	

gta atg aga aac gac ggg tta tta atc tca tct gtt atg ata aat ggc 528
Val Met Arg Asn Asp Gly Leu Leu Ile Ser Ser Val Met Ile Asn Gly
165 170 175

tgt tac aat gtc ata cta aat gat ata caa gca gaa cct tac ata tgt 576
Cys Tyr Asn Val Ile Leu Asn Asp Ile Gln Ala Glu Pro Tyr Ile Cys
180 185 190

gca gga cta gga gga gat ttt ata gaa ttc ttc aat ggc ttt cat gtt 624
Ala Gly Leu Gly Gly Asp Phe Ile Glu Phe Phe Asn Gly Phe His Val
195 200 205

aag cta gct tat caa ggt aaa gta ggc att agt tat caa ata ttc cct 672
Lys Leu Ala Tyr Gln Gly Lys Val Gly Ile Ser Tyr Gln Ile Phe Pro
210 215 220

gaa gta aga tta ttt att gat gga tac tac cat aaa gta aaa ggc aac 720
Glu Val Arg Leu Phe Ile Asp Gly Tyr Tyr His Lys Val Lys Gly Asn
225 230 235 240

aag ttt aaa aat tta cac gtt caa cat gta ggt gca ctt gca gca ctc 768
Lys Phe Lys Asn Leu His Val Gln His Val Gly Ala Leu Ala Ala Leu
245 250 255

cct aaa gtt aca tct gca gtt gca aca ctt aat att gga tac ttt ggt 816
Pro Lys Val Thr Ser Ala Val Ala Thr Leu Asn Ile Gly Tyr Phe Gly
260 265 270

tgt gaa gct gga gta aga ttc ata ttt taa 846
Cys Glu Ala Gly Val Arg Phe Ile Phe
275 280

<210> 58
<211> 281
<212> PRT
<213> p30-9

<400> 58
Met Asn Asn Lys Arg Asn Phe Phe Leu Ile Gly Met Ser Leu Leu Ile
1 5 10 15

Asn Leu Leu Leu Pro Ile Asp Ala Ser Ser Met Glu Val His Asn Tyr
20 25 30

Thr His Phe Thr Pro Arg Leu Tyr Ile Ser Gly Gln Tyr Arg Pro Gly
35 40 45

Val Ser His Phe Ser Lys Phe Ser Val Lys Glu Thr His Cys Asn Thr
50 55 60

Val Gln Leu Val Gly Leu Thr Lys Asp Ile Lys Val Thr Asn Asn Ser
65 70 75 80

Ser Ile Asn Thr Asn Thr Ser Phe Asn Phe Pro Tyr Val Ala Glu Phe
85 90 95

Gln Asp Asn Ala Met Ser Phe Ser Gly Ala Ile Gly Cys Phe Tyr Ser
100 105 110

Glu His Phe Arg Ile Glu Val Glu Ala Ser Tyr Glu Glu Phe Asp Val
115 120 125

Lys Asn Pro Glu Gly Ser Thr Thr Asp Ser Tyr Arg Tyr Phe Ala Leu
130 135 140

Ala Arg Gly Met Asp Gly Asn Asn Ile Pro Thr Ser Gln Lys Phe Thr
145 150 155 160

Val Met Arg Asn Asp Gly Leu Leu Ile Ser Ser Val Met Ile Asn Gly
165 170 175

Cys Tyr Asn Val Ile Leu Asn Asp Ile Gln Ala Glu Pro Tyr Ile Cys
180 185 190

Ala Gly Leu Gly Gly Asp Phe Ile Glu Phe Phe Asn Gly Phe His Val
195 200 205

Lys Leu Ala Tyr Gln Gly Lys Val Gly Ile Ser Tyr Gln Ile Phe Pro
210 215 220

Glu Val Arg Leu Phe Ile Asp Gly Tyr Tyr His Lys Val Lys Gly Asn
225 230 235 240

Lys Phe Lys Asn Leu His Val Gln His Val Gly Ala Leu Ala Ala Leu
245 250 255

Pro Lys Val Thr Ser Ala Val Ala Thr Leu Asn Ile Gly Tyr Phe Gly
260 265 270

Cys Glu Ala Gly Val Arg Phe Ile Phe
275 280

<210> 59

<211> 840
 <212> DNA
 <213> p30-11

<220>
 <221> CDS
 <222> (1)..(840)

<400> 59

atg aac aaa aag aaa att att aca gta gga aca aca tta gct tat tta	48
Met Asn Lys Lys Lys Ile Ile Thr Val Gly Thr Thr Leu Ala Tyr Leu	
1 5 10 15	
tta tta tca cct aac ata tct ttt tca gaa gta atc aac aat gat act	96
Leu Leu Ser Pro Asn Ile Ser Phe Ser Glu Val Ile Asn Asn Asp Thr	
20 25 30	
gat aaa tat tct aga cta tat ata agt ggt caa tat aaa cca gga ttt	144
Asp Lys Tyr Ser Arg Leu Tyr Ile Ser Gly Gln Tyr Lys Pro Gly Phe	
35 40 45	
tct tat ttt aat aag ttc tca gtt aga gaa act gat cat ttc act aaa	192
Ser Tyr Phe Asn Lys Phe Ser Val Arg Glu Thr Asp His Phe Thr Lys	
50 55 60	
gca tta ata gga tta aga cat gac gca ata tct act aaa aat tta aca	240
Ala Leu Ile Gly Leu Arg His Asp Ala Ile Ser Thr Lys Asn Leu Thr	
65 70 75 80	
act aat aca gat ttc aat act ctt tat aaa gta aca ttt caa aac aac	288
Thr Asn Thr Asp Phe Asn Thr Leu Tyr Lys Val Thr Phe Gln Asn Asn	
85 90 95	
atc att agc ttt agc ggt gct att ggt tat tct gat agc aca ggt gta	336
Ile Ile Ser Phe Ser Gly Ala Ile Gly Tyr Ser Asp Ser Thr Gly Val	
100 105 110	
agg ttt gag cta gaa ggc tct tat gaa gag ttc gat gtt aca gac cct	384
Arg Phe Glu Leu Glu Gly Ser Tyr Glu Glu Phe Asp Val Thr Asp Pro	
115 120 125	
gga gat tgt ata ata aaa gat act tac agg tac ttt gca tta gct aga	432
Gly Asp Cys Ile Ile Lys Asp Thr Tyr Arg Tyr Phe Ala Leu Ala Arg	
130 135 140	
aaa aca agt ggt aat cat ccc aac gat aat ggg gaa tat act gtc atg	480
Lys Thr Ser Gly Asn His Pro Asn Asp Asn Gly Glu Tyr Thr Val Met	
145 150 155 160	

aga aat gat gga gta tcc att acc tcc gtt ata ttc aat ggt tgt tat 528
 Arg Asn Asp Gly Val Ser Ile Thr Ser Val Ile Phe Asn Gly Cys Tyr
 165 170 175

gat ctc tct tta aaa gag cta gaa ata tca cca tat gtt tgc att ggt 576
 Asp Leu Ser Leu Lys Glu Leu Glu Ile Ser Pro Tyr Val Cys Ile Gly
 180 185 190

atc gga gga gac ttt ata gaa ttt ttt gat gct tta cac att aaa tta 624
 Ile Gly Gly Asp Phe Ile Glu Phe Phe Asp Ala Leu His Ile Lys Leu
 195 200 205

gca tat caa ggt aaa cta ggt att agc tat tct ttt tcc act aga aca 672
 Ala Tyr Gln Gly Lys Leu Gly Ile Ser Tyr Ser Phe Ser Thr Arg Thr
 210 215 220

aat tta ttt atc gat tgt tat tac cat aga gtt ata ggt aat caa ttt 720
 Asn Leu Phe Ile Asp Cys Tyr Tyr His Arg Val Ile Gly Asn Gln Phe
 225 230 235 240

aat aat tta aat gtt caa cat gta gtt gag ctt aca gaa gca cct aaa 768
 Asn Asn Leu Asn Val Gln His Val Val Glu Leu Thr Glu Ala Pro Lys
 245 250 255

gct aca tct gca att gct aca ctt aat gtt agt tac ttc ggt gga gaa 816
 Ala Thr Ser Ala Ile Ala Thr Leu Asn Val Ser Tyr Phe Gly Gly Glu
 260 265 270

gtt-gga att aga ctt atg ttt taa 840
 Val-Gly Ile Arg Leu Met Phe
 275 280

<210> 60
 <211> 279
 <212> PRT
 <213> p30-11

<400> 60
 Met Asn Lys Lys Lys Ile Ile Thr Val Gly Thr Thr Leu Ala Tyr Leu
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Leu Leu Ser Pro Asn Ile Ser Phe Ser Glu Val Ile Asn Asn Asp Thr
 20 25 30

Asp Lys Tyr Ser Arg Leu Tyr Ile Ser Gly Gln Tyr Lys Pro Gly Phe
 35 40 45

Ser Tyr Phe Asn Lys Phe Ser Val Arg Glu Thr Asp His Phe Thr Lys
 50 55 60
 Ala Leu Ile Gly Leu Arg His Asp Ala Ile Ser Thr Lys Asn Leu Thr
 65 70 75 80
 Thr Asn Thr Asp Phe Asn Thr Leu Tyr Lys Val Thr Phe Gln Asn Asn
 85 90 95
 Ile Ile Ser Phe Ser Gly Ala Ile Gly Tyr Ser Asp Ser Thr Gly Val
 100 105 110
 Arg Phe Glu Leu Glu Gly Ser Tyr Glu Glu Phe Asp Val Thr Asp Pro
 115 120 125
 Gly Asp Cys Ile Ile Lys Asp Thr Tyr Arg Tyr Phe Ala Leu Ala Arg
 130 135 140
 Lys Thr Ser Gly Asn His Pro Asn Asp Asn Gly Glu Tyr Thr Val Met
 145 150 155 160
 Arg Asn Asp Gly Val Ser Ile Thr Ser Val Ile Phe Asn Gly Cys Tyr
 165 170 175
 Asp Leu Ser Leu Lys Glu Leu Glu Ile Ser Pro Tyr Val Cys Ile Gly
 180 185 190
 Ile Gly Gly Asp Phe Ile Glu Phe Phe Asp Ala Leu His Ile Lys Leu
 195 200 205
 Ala Tyr Gln Gly Lys Leu Gly Ile Ser Tyr Ser Phe Ser Thr Arg Thr
 210 215 220
 Asn Leu Phe Ile Asp Cys Tyr Tyr His Arg Val Ile Gly Asn Gln Phe
 225 230 235 240
 Asn Asn Leu Asn Val Gln His Val Val Glu Leu Thr Glu Ala Pro Lys
 245 250 255
 Ala Thr Ser Ala Ile Ala Thr Leu Asn Val Ser Tyr Phe Gly Gly Glu
 260 265 270
 Val Gly Ile Arg Leu Met Phe
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<210> 61

<211> 726
 <212> DNA
 <213> p30-12

<220>
 <221> CDS
 <222> (1)..(726)

<400> 61

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Pro Val Val Ser His Tyr Ser Asp Phe Ser Ile Lys Glu Thr Tyr Thr	
1 5 10 15	
aac act gag gca ttg ttt ggg cta aaa caa gat att agt tct att tta	96
Asn Thr Glu Ala Leu Phe Gly Leu Lys Gln Asp Ile Ser Ser Ile Leu	
20 25 30	
cgt aat aaa gag acc aca caa tat aat aac aat ttt aac gtt ccc tat	144
Arg Asn Lys Glu Thr Thr Gln Tyr Asn Asn Asn Phe Asn Val Pro Tyr	
35 40 45	
act gca aaa ttt caa gac gac ttt ggc agt ttc agc ata gct gtt gga	192
Thr Ala Lys Phe Gln Asp Asp Phe Ala Ser Phe Ser Ile Ala Val Gly	
50 55 60	
tat att gct aac aat ggt cca aga att gaa ata gaa gga tct tac gaa	240
Tyr Ile Ala Asn Asn Gly Pro Arg Ile Glu Ile Glu Gly Ser Tyr Glu	
65 70 75 80	
gaa ttt gat gtt aaa aac cca gga aat tat aca aca ata gat gct cat	288
Glu Phe Asp Val Lys Asn Pro Gly Asn Tyr Thr Thr Ile Asp Ala His	
85 90 95	
agg tac att gct tta gct aga gaa aaa act tct tac tat cta agt tct	336
Arg Tyr Ile Ala Leu Ala Arg Glu Lys Thr Ser Tyr Tyr Leu Ser Ser	
100 105 110	
cct aaa gaa aac aaa tat gta att ata aag aat aac ggc ata tct att	384
Pro Lys Glu Asn Lys Tyr Val Ile Ile Lys Asn Asn Gly Ile Ser Ile	
115 120 125	
gta tct att ata att aat ggt tgt tat gat att tct tta aat gat tct	432
Val Ser Ile Ile Ile Asn Gly Cys Tyr Asp Ile Ser Leu Asn Asp Ser	
130 135 140	
aag gtg tca cct tac ata tgc aca ggg ttt ggt gga gat ttt ata gag	480
Lys Val Ser Pro Tyr Ile Cys Thr Gly Phe Gly Gly Asp Phe Ile Glu	
145 150 155 160	

ttt ttt agt gct ata cgt ttt aag ttt gct tat caa ggt aaa ata ggt 528
Phe Phe Ser Ala Ile Arg Phe Lys Phe Ala Tyr Gln Gly Lys Ile Gly
165 170 175

atc agt tat tca tta tct tct aac ata att tta ttt act gat gga tat 576
Ile Ser Tyr Ser Leu Ser Ser Asn Ile Ile Leu Phe Thr Asp Gly Tyr
180 185 190

tac cac aag gta ata aat tcc caa ttt aaa aat tta aat gtt gaa cat 624
Tyr His Lys Val Ile Asn Ser Gln Phe Lys Asn Leu Asn Val Glu His
195 200 205

gtt gtt aat gag tta act aca gat cct aaa gtg act tct gca aca gca 672
Val Val Asn Glu Leu Thr Thr Asp Pro Lys Val Thr Ser Ala Thr Ala
210 215 220

ttt ctt aat att gag tat ttt ggt ggt gaa ttt gga tta aaa ttt ata 720
Phe Leu Asn Ile Glu Tyr Phe Gly Gly Glu Phe Gly Leu Lys Phe Ile
225 230 235 240

ttt taa 726
Phe

<210> 62
<211> 241
<212> PRT
<213> p30-12

<400> 62

Pro Val Val Ser His Tyr Ser Asp Phe Ser Ile Lys Glu Thr Tyr Thr
1 5 10 15

Asn Thr Glu Ala Leu Phe Gly Leu Lys Gln Asp Ile Ser Ser Ile Leu
20 25 30

Arg Asn Lys Glu Thr Thr Gln Tyr Asn Asn Asn Phe Asn Val Pro Tyr
35 40 45

Thr Ala Lys Phe Gln Asp Asp Phe Ala Ser Phe Ser Ile Ala Val Gly
50 55 60

Tyr Ile Ala Asn Asn Gly Pro Arg Ile Glu Ile Glu Gly Ser Tyr Glu
65 70 75 80

Glu Phe Asp Val Lys Asn Pro Gly Asn Tyr Thr Thr Ile Asp Ala His
85 90 95

Arg Tyr Ile Ala Leu Ala Arg Glu Lys Thr Ser Tyr Tyr Leu Ser Ser
100 105 110

Pro Lys Glu Asn Lys Tyr Val Ile Ile Lys Asn Asn Gly Ile Ser Ile
115 120 125

Val Ser Ile Ile Ile Asn Gly Cys Tyr Asp Ile Ser Leu Asn Asp Ser
130 135 140

Lys Val Ser Pro Tyr Ile Cys Thr Gly Phe Gly Gly Asp Phe Ile Glu
145 150 155 160

Phe Phe Ser Ala Ile Arg Phe Lys Phe Ala Tyr Gln Gly Lys Ile Gly
165 170 175

Ile Ser Tyr Ser Leu Ser Ser Asn Ile Ile Leu Phe Thr Asp Gly Tyr
180 185 190

Tyr His Lys Val Ile Asn Ser Gln Phe Lys Asn Leu Asn Val Glu His
195 200 205

Val Val Asn Glu Leu Thr Thr Asp Pro Lys Val Thr Ser Ala Thr Ala
210 215 220

Phe Leu Asn Ile Glu Tyr Phe Gly Gly Glu Phe Gly Leu Lys Phe Ile
225 230 235 240

Phe

<210> 63

<211> 19

<212> PRT

<213> N-terminal of OMP-1 protein

<400> 63

Asp Pro Ala Gly Ser Gly Ile Asn Gly Asn Phe Tyr Ile Ser Gly Lys
1 5 10 15

Tyr Met Pro

<210> 64

<211> 45

<212> DNA

<213> FECH1

<400> 64

cgggatccga attcggatgc atatcaatcg gatgcaatct ttcta

45

<210> 65

<211> 36

<212> DNA

<213> RECH2

<400> 65

agcggccgct taagaatcac gagaactctt cgctcc

36

<210> 66

<211> 20

<212> DNA

<213> REC1

<400> 66

acctaacttt ccttggttaag

20